

**SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-2.szlm60.rnpbm.**

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
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start

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

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Run on:      July 26, 2006, 15:59:07 ; Search time 622.366 Seconds
              (without alignments)
              375.125 Million cell updates/sec
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Title:      US-10-743-384-2
Perfect score: 19
Sequence:   1 tgcgggacttaacccaaca 19
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24217294

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Minimum DB seq length: 0
Maximum DB seq length: 60
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 60 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					
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c	2	19	100.0	19	7	US-10-085-134A-8	Sequence 8, Appli
	3	19	100.0	19	9	US-10-743-384-2	Sequence 2, Appli
c	4	19	100.0	19	9	US-10-743-384-8	Sequence 8, Appli
	5	19	100.0	20	6	US-10-233-223-3	Sequence 3, Appli
	6	19	100.0	21	3	US-09-726-774-25	Sequence 25, Appl
	7	19	100.0	21	8	US-10-719-633-25	Sequence 25, Appl
	8	19	100.0	25	6	US-10-020-596-3	Sequence 3, Appli
	9	19	100.0	25	8	US-10-712-525-3	Sequence 3, Appli
c	10	19	100.0	25	9	US-10-660-122-10	Sequence 10, Appl
	11	19	100.0	26	3	US-09-736-151-4	Sequence 4, Appli
	12	19	100.0	26	3	US-09-736-151-5	Sequence 5, Appli
	13	19	100.0	26	3	US-09-736-151-6	Sequence 6, Appli
	14	19	100.0	26	3	US-09-736-151-7	Sequence 7, Appli
	15	19	100.0	26	3	US-09-736-151-8	Sequence 8, Appli
	16	19	100.0	26	3	US-09-736-151-9	Sequence 9, Appli
	17	19	100.0	26	3	US-09-808-558-1	Sequence 1, Appli
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c	20	19	100.0	26	6	US-10-020-596-2	Sequence 2, Appli
c	21	19	100.0	26	6	US-10-233-223-1	Sequence 1, Appli
	22	19	100.0	26	6	US-10-233-223-2	Sequence 2, Appli
	23	19	100.0	26	8	US-10-712-525-1	Sequence 1, Appli
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c	25	19	100.0	26	10	US-10-973-162-1	Sequence 1, Appli
	26	19	100.0	26	10	US-10-973-162-2	Sequence 2, Appli
	27	19	100.0	26	10	US-10-973-162-3	Sequence 3, Appli
	28	19	100.0	26	10	US-10-973-162-4	Sequence 4, Appli
	29	19	100.0	26	10	US-10-973-162-5	Sequence 5, Appli
	30	19	100.0	26	10	US-10-973-162-6	Sequence 6, Appli
	31	19	100.0	26	10	US-10-973-162-7	Sequence 7, Appli
c	32	19	100.0	26	10	US-10-973-162-8	Sequence 8, Appli
c	33	19	100.0	26	10	US-10-973-162-9	Sequence 9, Appli
	34	19	100.0	26	10	US-10-973-162-10	Sequence 10, Appl
	35	19	100.0	26	10	US-10-973-162-11	Sequence 11, Appl
c	36	19	100.0	59	2	US-08-781-986A-4958	Sequence 4958, Ap
c	37	19	100.0	59	8	US-10-329-624-4958	Sequence 4958, Ap
c	38	18	94.7	19	9	US-10-660-122-168	Sequence 168, App
c	39	18	94.7	19	9	US-10-660-122-234	Sequence 234, App
c	40	18	94.7	19	9	US-10-660-122-238	Sequence 238, App
c	41	18	94.7	19	9	US-10-660-122-240	Sequence 240, App
c	42	18	94.7	55	6	US-10-223-126-188	Sequence 188, App
c	43	18	94.7	55	15	US-11-070-519-188	Sequence 188, App
c	44	17.4	91.6	30	9	US-10-660-122-8	Sequence 8, Appli
c	45	16	84.2	20	11	US-10-831-286A-34358	Sequence 34358, A
c	46	15.4	81.1	25	11	US-10-933-982-5997	Sequence 5997, Ap
	47	14.4	75.8	19	11	US-10-310-914A-1106917	Sequence 1106917,
c	48	14.4	75.8	60	3	US-09-908-975-23315	Sequence 23315, A
c	49	14.2	74.7	24	11	US-10-310-914A-267576	Sequence 267576,
	50	14.2	74.7	25	8	US-10-719-956-527124	Sequence 527124,
	51	14.2	74.7	25	8	US-10-719-956-528344	Sequence 528344,
	52	14.2	74.7	25	13	US-11-036-317-93252	Sequence 93252, A
c	53	14.2	74.7	25	16	US-11-136-527-345597	Sequence 345597,
c	54	14.2	74.7	25	16	US-11-136-527-345598	Sequence 345598,
	55	14	73.7	15	10	US-10-697-802A-118	Sequence 118, App
	56	14	73.7	16	10	US-10-697-802A-119	Sequence 119, App
	57	14	73.7	17	10	US-10-697-802A-123	Sequence 123, App
	58	14	73.7	18	10	US-10-697-802A-124	Sequence 124, App
	59	14	73.7	19	10	US-10-697-802A-132	Sequence 132, App
	60	14	73.7	20	10	US-10-697-802A-133	Sequence 133, App

## ALIGNMENTS

## RESULT 1

US-10-085-134A-2

; Sequence 2, Application US/10085134A

; Publication No. US20030124545A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, Richard

; APPLICANT: Yang, Samuel

; APPLICANT: Lin, Shin

; APPLICANT: Kelen, Gabor

; TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of

; TITLE OF INVENTION: Bacterial Infections

; FILE REFERENCE: 001107.00234

; CURRENT APPLICATION NUMBER: US/10/085,134A  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/272,642  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-085-134A-2

Query Match 100.0%; Score 19; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGGGACTTAACCCAACA 19  
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Db 1 TCGGGGACTTAACCCAACA 19

## RESULT 2

US-10-085-134A-8/c

; Sequence 8, Application US/10085134A  
; Publication No. US2003012454A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, Richard  
; APPLICANT: Yang, Samuel  
; APPLICANT: Lin, Shin  
; APPLICANT: Kelen, Gabor  
; TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of  
; TITLE OF INVENTION: Bacterial Infections  
; FILE REFERENCE: 001107.00234  
; CURRENT APPLICATION NUMBER: US/10/085,134A  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/272,642  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-085-134A-8

Query Match 100.0%; Score 19; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGGGACTTAACCCAACA 19  
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Db 19 TCGGGGACTTAACCCAACA 1

## RESULT 3

US-10-743-384-2

; Sequence 2, Application US/10743384  
; Publication No. US20040235010A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, Richard  
; APPLICANT: Yang, Samuel  
; APPLICANT: Lin, Shin  
; APPLICANT: Kelen, Gabor  
; TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of  
; TITLE OF INVENTION: Bacterial Infections  
; FILE REFERENCE: 001107.00234  
; CURRENT APPLICATION NUMBER: US/10/743,384  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: US/10/085,134A  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/272,642  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 19

; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-743-384-2

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 1 TGCGGGACTTAACCCAACA 19

## RESULT 4

US-10-743-384-8/c

; Sequence 8, Application US/10743384  
; Publication No. US20040235010A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, Richard  
; APPLICANT: Yang, Samuel  
; APPLICANT: Lin, Shin  
; APPLICANT: Kelen, Gabor  
; TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of  
; TITLE OF INVENTION: Bacterial Infections  
; FILE REFERENCE: 001107.00234  
; CURRENT APPLICATION NUMBER: US/10/743,384  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: US/10/085,134A  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/272,642  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-743-384-8

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 19 TGCGGGACTTAACCCAACA 1

## RESULT 5

US-10-233-223-3

; Sequence 3, Application US/10233223  
; Publication No. US20030105320A1  
; GENERAL INFORMATION:  
; APPLICANT: Becker, Michael M.  
; APPLICANT: Nelson, No. US20030105320A1man C.  
; TITLE OF INVENTION: Affinity-Shifted Probes for Quantifying  
; TITLE OF INVENTION: Analyte Polynucleotides  
; FILE REFERENCE: GP129-03.UT  
; CURRENT APPLICATION NUMBER: US/10/233,223  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 60/316,770  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 60/368,072  
; PRIOR FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: E. coli  
US-10-233-223-3

Query Match 100.0%; Score 19; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 1 TGCGGGACTTAACCCAACA 19

## RESULT 6

US-09-726-774-25  
; Sequence 25, Application US/09726774  
; Patent No. US20020082226A1  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Antisense Antibacterial Method and  
; TITLE OF INVENTION: Composition  
; FILE REFERENCE: 0450-0032.30  
; CURRENT APPLICATION NUMBER: US/09/726,774  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 60/168,150  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense oligomer  
US-09-726-774-25

Query Match 100.0%; Score 19; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 2 TGCGGGACTTAACCCAACA 20

## RESULT 7

US-10-719-633-25  
; Sequence 25, Application US/10719633  
; Publication No. US20040137485A1  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Antisense Antibacterial Method and  
; TITLE OF INVENTION: Composition  
; FILE REFERENCE: 0450-0032.30  
; CURRENT APPLICATION NUMBER: US/10/719,633  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US/09/726,774  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 60/168,150  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense oligomer  
US-10-719-633-25

Query Match 100.0%; Score 19; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 2 TGCGGGACTTAACCCAACA 20

## RESULT 8

US-10-020-596-3  
; Sequence 3, Application US/10020596  
; Publication No. US20020164614A1  
; GENERAL INFORMATION:

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; APPLICANT: BECKER, Michael M.
; TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
; FILE REFERENCE: GP123-02.UT
; CURRENT APPLICATION NUMBER: US/10/020,596
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/255,535
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-020-596-3

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Query Match 100.0%; Score 19; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 6 TGCGGGACTTAACCCAACA 24

## RESULT 9

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US-10-712-525-3
; Sequence 3, Application US/10712525
; Publication No. US20040077014A1
; GENERAL INFORMATION:
; APPLICANT: BECKER, Michael M.
; TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
; FILE REFERENCE: GP123-02.UT
; CURRENT APPLICATION NUMBER: US/10/712,525
; CURRENT FILING DATE: 2200-11-01
; PRIOR APPLICATION NUMBER: US/10/020,596
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/255,535
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-712-525-3

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Query Match 100.0%; Score 19; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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 Db 6 TGCGGGACTTAACCCAACA 24

RESULT 10

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US-10-660-122-10/c
; Sequence 10, Application US/10660122
; Publication No. US20040219517A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeil, John
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Methods For Rapid Identification Of Pathogens In Humans And Animals
; FILE REFERENCE: IBIS0061-100
; CURRENT APPLICATION NUMBER: US/10/660,122
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 10/323,233
; PRIOR FILING DATE: 2002-12-18
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; PRIOR APPLICATION NUMBER: 09/798,007
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/431,319
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/443,443
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/443,788
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 60/447,529
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-660-122-10
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Query Match          100.0%; Score 19; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TGC GGGACTTAACCCAACA 19
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Db      20 TGC GGGACTTAACCCAACA 2
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#### RESULT 11

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US-09-736-151-4
; Sequence 4, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-4
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Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TGC GGGACTTAACCCAACA 19
          |||||
Db      7 TGC GGGACTTAACCCAACA 25
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#### RESULT 12

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US-09-736-151-5
; Sequence 5, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
```

```
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the
; OTHER INFORMATION: phosphate between nucleotides at positions 16 and
; OTHER INFORMATION: 17 is a thiophosphate
US-09-736-151-5
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Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TGCGGGACTTAACCCAACA 19
        |||
Db      7 TGCGGGACTTAACCCAACA 25
```

RESULT 13

```
US-09-736-151-6
; Sequence 6, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the
; OTHER INFORMATION: phosphate at the 3' end is a terminal
; OTHER INFORMATION: thiophosphate
US-09-736-151-6
```

```
Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TGCGGGACTTAACCCAACA 19
        |||
Db      7 TGCGGGACTTAACCCAACA 25
```

RESULT 14

```
US-09-736-151-7
; Sequence 7, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the
; OTHER INFORMATION: phosphate between the two nucleotides at position
; OTHER INFORMATION: 16 and 17 is a thiophosphate
US-09-736-151-7
```

```
Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TGC GGGACTTAACCCAACA 19
        :|||||||:|||||||
Db      7 UGCGGGACUUAACCCAACA 25
```

#### RESULT 15

```
US-09-736-151-8
; Sequence 8, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the
; OTHER INFORMATION: phosphate at the 3' end is a terminal
; OTHER INFORMATION: thiophosphate
US-09-736-151-8
```

```
Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TGC GGGACTTAACCCAACA 19
        :|||||||:|||||||
Db      7 UGCGGGACUUAACCCAACA 25
```

#### RESULT 16

US-09-736-151-9  
; Sequence 9, Application US/09736151  
; Patent No. US20020081586A1  
; GENERAL INFORMATION:  
; APPLICANT: LAAYOUN, ALI  
; APPLICANT: MENOUE, LIONEL  
; APPLICANT: TORA, CHRISTELLE  
; APPLICANT: BANERJEE, ALOKE R.  
; APPLICANT: BECKER, MICHAEL M.  
; APPLICANT: BROWNE, KENNETH A.  
; APPLICANT: FRIEDENBERG, MATTHEW C.  
; APPLICANT: HAJJAR, FRED F.  
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID  
; FILE REFERENCE: 104959  
; CURRENT APPLICATION NUMBER: US/09/736,151  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/172,136  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:primer  
US-09-736-151-9

Query Match 100.0%; Score 19; DB 3; Length 26;  
Best Local Similarity 84.2%; Pred. No. 5.9;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGGGACTTAACCCAACA 19  
:|||||||:|||||||  
Db 7 UGCGGGACUUAACCCAACA 25

RESULT 17

US-09-808-558-1  
; Sequence 1, Application US/09808558  
; Publication No. US20030036058A1  
; GENERAL INFORMATION:  
; APPLICANT: Becker, Michael M.  
; Majlessi, Mehrdad  
; TITLE OF INVENTION: METHODS FOR DETECTING AND  
; AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED  
; OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gen-Probe Incorporated  
; STREET: 10210 Genetic Center Drive  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/808,558  
; FILING DATE: 14-Mar-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,300  
; FILING DATE: 15-JUL-1997  
; APPLICATION NUMBER: 60/021,818  
; FILING DATE: 15-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cappellari, Charles B  
; REGISTRATION NUMBER: 40,937  
; REFERENCE/DOCKET NUMBER: CHE7B-P01A01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-410-8927  
; TELEFAX: 619-410-8928

```
;
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 26 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-808-558-1
```

```
Query Match      100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TGC GGGACTTAACCCAACA 19
        |||
Db      7 TGC GGGACTTAACCCAACA 25
```

# RESULT 18

US-09-808-558-2/c

; Sequence 2, Application US/09808558

; Publication No. US20030036058A1

; GENERAL INFORMATION:

; APPLICANT: Becker, Michael M.

; Majlessi, Mehrdad

; TITLE OF INVENTION: METHODS FOR DETECTING AND

; AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED

; OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gen-Probe Incorporated

; STREET: 10210 Genetic Center Drive

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/808,558

; FILING DATE: 14-Mar-2001

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/893,300

; FILING DATE: 15-JUL-1997

; APPLICATION NUMBER: 60/021,818

; FILING DATE: 15-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Cappellari, Charles B

; REGISTRATION NUMBER: 40,937

; REFERENCE/DOCKET NUMBER: CHE7B-P01A01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-410-8927

; TELEFAX: 619-410-8928

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-808-558-2

```
Query Match      100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TGC GGGACTTAACCCAACA 19
        |||
Db     20 TGC GGGACTTAACCCAACA 2
```

RESULT 19

US-10-020-596-1

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; Sequence 1, Application US/10020596
; Publication No. US20020164614A1
; GENERAL INFORMATION:
; APPLICANT: BECKER, Michael M.
; TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
; FILE REFERENCE: GP123-02.UT
; CURRENT APPLICATION NUMBER: US/10/020,596
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/255,535
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-020-596-1
```

```
Query Match          100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TGC GGGACTTAACCCAACA 19
          |||||
Db       7 TGC GGGACTTAACCCAACA 25
```

RESULT 20

US-10-020-596-2/c

```
; Sequence 2, Application US/10020596
; Publication No. US20020164614A1
; GENERAL INFORMATION:
; APPLICANT: BECKER, Michael M.
; TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
; FILE REFERENCE: GP123-02.UT
; CURRENT APPLICATION NUMBER: US/10/020,596
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/255,535
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-020-596-2
```

```
Query Match          100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TGC GGGACTTAACCCAACA 19
          |||||
Db       20 TGC GGGACTTAACCCAACA 2
```

Search completed: July 26, 2006, 17:25:39  
Job time : 623.366 secs

SCORE 1.3 BuildDate: 12/06/2005

# SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384- 2.szm60.rni.

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 15:54:56 ; Search time 70.439 Seconds  
(without alignments)  
504.707 Million cell updates/sec

Title: US-10-743-384-2  
Perfect score: 19  
Sequence: 1 tgcgggacttaaccaaca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1475510

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 60 summaries

Database : Issued Patents NA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
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6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	19	100.0	19	3	US-10-085-134A-2
c 2	19	100.0	19	3	US-10-085-134A-8
3	19	100.0	21	3	US-09-726-774-25
4	19	100.0	26	2	US-08-478-221-5
c 5	19	100.0	26	2	US-08-478-221-6
6	19	100.0	26	2	US-08-478-221-11
c 7	19	100.0	26	2	US-08-478-221-12

c	8	19	100.0	26	2	US-08-475-334-1	Sequence 1, Appli
c	9	19	100.0	26	2	US-08-475-334-2	Sequence 2, Appli
	10	19	100.0	26	3	US-09-094-139-1	Sequence 1, Appli
c	11	19	100.0	26	3	US-09-094-139-2	Sequence 2, Appli
	12	19	100.0	26	3	US-08-893-300-1	Sequence 1, Appli
c	13	19	100.0	26	3	US-08-893-300-2	Sequence 2, Appli
	14	19	100.0	26	3	US-09-736-151-4	Sequence 4, Appli
	15	19	100.0	26	3	US-09-736-151-5	Sequence 5, Appli
	16	19	100.0	26	3	US-09-736-151-6	Sequence 6, Appli
	17	19	100.0	26	3	US-09-736-151-7	Sequence 7, Appli
	18	19	100.0	26	3	US-09-736-151-8	Sequence 8, Appli
	19	19	100.0	26	3	US-09-736-151-9	Sequence 9, Appli
c	20	19	100.0	26	3	US-09-523-237B-1	Sequence 1, Appli
	21	19	100.0	26	3	US-09-523-237B-2	Sequence 2, Appli
	22	19	100.0	26	3	US-09-523-237B-3	Sequence 3, Appli
	23	19	100.0	26	3	US-09-523-237B-4	Sequence 4, Appli
	24	19	100.0	26	3	US-09-523-237B-5	Sequence 5, Appli
	25	19	100.0	26	3	US-09-523-237B-6	Sequence 6, Appli
	26	19	100.0	26	3	US-09-523-237B-7	Sequence 7, Appli
c	27	19	100.0	26	3	US-09-523-237B-8	Sequence 8, Appli
c	28	19	100.0	26	3	US-09-523-237B-9	Sequence 9, Appli
	29	19	100.0	26	3	US-09-523-237B-10	Sequence 10, Appli
	30	19	100.0	26	3	US-09-523-237B-11	Sequence 11, Appli
c	31	19	100.0	59	3	US-08-956-171E-4958	Sequence 4958, Ap
c	32	19	100.0	59	3	US-08-781-986A-4958	Sequence 4958, Ap
c	33	14	73.7	18	3	US-09-073-465-12	Sequence 12, Appli
	34	14	73.7	18	3	US-09-073-465-13	Sequence 13, Appli
c	35	14	73.7	22	2	US-08-244-269-46	Sequence 46, Appli
c	36	14	73.7	22	2	US-07-923-871C-26	Sequence 26, Appli
c	37	14	73.7	22	3	US-09-634-960A-38	Sequence 38, Appli
c	38	14	73.7	22	7	PCT-US91-01574-26	Sequence 26, Appli
	39	14	73.7	25	2	US-08-743-637B-272	Sequence 272, App
	40	13.4	70.5	22	3	US-09-700-486-5	Sequence 5, Appli
	41	13.2	69.5	51	3	US-09-989-002-49	Sequence 49, Appli
	42	13	68.4	21	3	US-09-726-774-28	Sequence 28, Appli
c	43	12.8	67.4	18	10	5180819-5	Patent No. 5180819
	44	12.8	67.4	18	10	5180819-8	Patent No. 5180819
	45	12.8	67.4	20	3	US-09-357-071-22	Sequence 22, Appli
	46	12.8	67.4	26	3	US-09-989-002-23	Sequence 23, Appli
	47	12.2	64.2	50	3	US-10-131-827-4842	Sequence 4842, Ap
	48	12.2	64.2	50	5	US-10-131-831-4842	Sequence 4842, Ap
	49	12	63.2	28	3	US-09-549-848B-73	Sequence 73, Appli
	50	12	63.2	28	3	US-09-688-069-73	Sequence 73, Appli
	51	12	63.2	33	3	US-09-609-133F-4	Sequence 4, Appli
c	52	12	63.2	40	3	US-09-495-066-7	Sequence 7, Appli
c	53	11.8	62.1	22	3	US-08-714-918-109	Sequence 109, App
c	54	11.8	62.1	22	3	US-09-265-315-109	Sequence 109, App
c	55	11.8	62.1	22	3	US-09-265-315-109	Sequence 109, App
c	56	11.8	62.1	22	3	US-09-266-417-109	Sequence 109, App
c	57	11.8	62.1	22	3	US-09-528-709-109	Sequence 109, App
c	58	11.8	62.1	22	3	US-09-527-745-109	Sequence 109, App
c	59	11.8	62.1	50	3	US-10-131-827-1522	Sequence 1522, Ap
c	60	11.8	62.1	50	5	US-10-131-831-1522	Sequence 1522, Ap

## ALIGNMENTS

## RESULT 1

US-10-085-134A-2

; Sequence 2, Application US/10085134A

; Patent No. 6699670

; GENERAL INFORMATION:

; APPLICANT: Rothman, Richard

; APPLICANT: Yang, Samuel

; APPLICANT: Lin, Shin

; APPLICANT: Kelen, Gabor

; TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of

; TITLE OF INVENTION: Bacterial Infections

; FILE REFERENCE: 001107.00234

; CURRENT APPLICATION NUMBER: US/10/085,134A

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: 60/272,642

; PRIOR FILING DATE: 2001-03-01

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-085-134A-2

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
|||||||  
Db 1 TGCGGGACTTAACCCAACA 19

## RESULT 2

US-10-085-134A-8/c  
; Sequence 8, Application US/10085134A  
; Patent No. 6699670  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, Richard  
; APPLICANT: Yang, Samuel  
; APPLICANT: Lin, Shin  
; APPLICANT: Kelen, Gabor  
; TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of  
; TITLE OF INVENTION: Bacterial Infections  
; FILE REFERENCE: 001107.00234  
; CURRENT APPLICATION NUMBER: US/10/085,134A  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/272,642  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-085-134A-8

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
|||||||  
Db 19 TGCGGGACTTAACCCAACA 1

## RESULT 3

US-09-726-774-25  
; Sequence 25, Application US/09726774  
; Patent No. 6677153  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Antisense Antibacterial Method and  
; TITLE OF INVENTION: Composition  
; FILE REFERENCE: 0450-0032.30  
; CURRENT APPLICATION NUMBER: US/09/726,774  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 60/168,150  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense oligomer  
US-09-726-774-25

Query Match 100.0%; Score 19; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19

Db                   |||||  
2 TGCGGGACTTAACCCAACA 20

## RESULT 4

US-08-478-221-5

; Sequence 5, Application US/08478221

; Patent No. 5731148

; GENERAL INFORMATION:

; APPLICANT: Michael Becker

; APPLICANT: No. 5731148man C. Nelson

; TITLE OF INVENTION: ADDUCT PROTECTION ASSAY

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/478,221

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:                   No. 5731148e

; ATTORNEY/AGENT INFORMATION:

; NAME: Heber, Sheldon O.

; REGISTRATION NUMBER: 38,179

; REFERENCE/DOCKET NUMBER: 209/190

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: nucleic acid

US-08-478-221-5

Query Match                   100.0%; Score 19; DB 2; Length 26;

Best Local Similarity       100.0%; Pred. No. 0.31;

Matches   19; Conservative   0; Mismatches   0; Indels    0; Gaps    0;

Qy                   1 TGCGGGACTTAACCCAACA 19

|||||

Db                   7 TGCGGGACTTAACCCAACA 25

## RESULT 5

US-08-478-221-6/c

; Sequence 6, Application US/08478221

; Patent No. 5731148

; GENERAL INFORMATION:

; APPLICANT: Michael Becker

; APPLICANT: No. 5731148man C. Nelson

; TITLE OF INVENTION: ADDUCT PROTECTION ASSAY

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

```

; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,221
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: No. 5731148e
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 209/190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
US-08-478-221-6

```

```

Query Match          100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 TGCGGGACTTAACCCAACA 19
        |||||
Db      20 TGCGGGACTTAACCCAACA 2

```

## RESULT 6

US-08-478-221-11

```

; Sequence 11, Application US/08478221
; Patent No. 5731148
; GENERAL INFORMATION:
; APPLICANT: Michael Becker
; APPLICANT: No. 5731148man C. Nelson
; TITLE OF INVENTION: ADDUCT PROTECTION ASSAY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,221
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: No. 5731148e
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 209/190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

```

; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: nucleic acid  
US-08-478-221-11

Query Match 100.0%; Score 19; DB 2; Length 26;  
Best Local Similarity 84.2%; Pred. No. 0.31;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
:|||||||:|||||||  
Db 7 UGCGGGACUUAACCCAACA 25

## RESULT 7

US-08-478-221-12/c  
; Sequence 12, Application US/08478221  
; Patent No. 5731148  
; GENERAL INFORMATION:  
; APPLICANT: Michael Becker  
; APPLICANT: No. 5731148man C. Nelson  
; TITLE OF INVENTION: ADDUCT PROTECTION ASSAY  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,221  
; FILING DATE: June 7, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below: No. 5731148e  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 209/190  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: nucleic acid  
US-08-478-221-12

Query Match 100.0%; Score 19; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
|||||||  
Db 20 TGCGGGACTTAACCCAACA 2

## RESULT 8

US-08-475-334-1

```

; Sequence 1, Application US/08475334
; Patent No. 5879885
; GENERAL INFORMATION:
;   APPLICANT: Becker, Michael M.
;   TITLE OF INVENTION: MICELLE PROTECTION ASSAY
;   NUMBER OF SEQUENCES: 13
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Gen-Probe Incorporated
;     STREET: 9880 Campus Point Drive
;     CITY: San Diego
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/475,334
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fisher, Carlos A
;     REGISTRATION NUMBER: 36,510
;     REFERENCE/DOCKET NUMBER: GP94009
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 619-535-2807
;     TELEFAX: 619-546-7929
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 26 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-08-475-334-1

```

```

Query Match          100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 TGCGGGACTTAACCCAACA 19
        |||||
Db      7 TGCGGGACTTAACCCAACA 25

```

## RESULT 9

US-08-475-334-2/c

```

; Sequence 2, Application US/08475334
; Patent No. 5879885
; GENERAL INFORMATION:
;   APPLICANT: Becker, Michael M.
;   TITLE OF INVENTION: MICELLE PROTECTION ASSAY
;   NUMBER OF SEQUENCES: 13
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Geh-Probe Incorporated
;     STREET: 9880 Campus Point Drive
;     CITY: San Diego
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/475,334
;     FILING DATE:
;     CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fisher, Carlos A  
; REGISTRATION NUMBER: 36,510  
; REFERENCE/DOCKET NUMBER: GP94009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-535-2807  
; TELEFAX: 619-546-7929  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-475-334-2

Query Match 100.0%; Score 19; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
|||||||  
Db 20 TGCGGGACTTAACCCAACA 2

## RESULT 10

US-09-094-139-1

; Sequence 1, Application US/09094139  
; Patent No. 6059561  
; GENERAL INFORMATION:  
; APPLICANT: Becker, Michael M.  
; TITLE OF INVENTION: MICELLE PROTECTION ASSAY  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gen-Probe Incorporated  
; STREET: 9880 Campus Point Drive  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/094,139  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,334  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fisher, Carlos A  
; REGISTRATION NUMBER: 36,510  
; REFERENCE/DOCKET NUMBER: GP94009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-535-2807  
; TELEFAX: 619-546-7929  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-094-139-1

Query Match 100.0%; Score 19; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19

Db                   |||||  
7 TGC GGGACTTAACCCAACA 25

## RESULT 11

US-09-094-139-2/c

; Sequence 2, Application US/09094139

; Patent No. 6059561

; GENERAL INFORMATION:

; APPLICANT: Becker, Michael M.

; TITLE OF INVENTION: MICELLE PROTECTION ASSAY

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gen-Probe Incorporated

; STREET: 9880 Campus Point Drive

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/094,139

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,334

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Fisher, Carlos A

; REGISTRATION NUMBER: 36,510

; REFERENCE/DOCKET NUMBER: GP94009

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-535-2807

; TELEFAX: 619-546-7929

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-094-139-2

Query Match                   100.0%; Score 19; DB 3; Length 26;

Best Local Similarity   100.0%; Pred. No. 0.31;

Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY                   1 TGC GGGACTTAACCCAACA 19

|||||

Db                   20 TGC GGGACTTAACCCAACA 2

## RESULT 12

US-08-893-300-1

; Sequence 1, Application US/08893300

; Patent No. 6130038

; GENERAL INFORMATION:

; APPLICANT: Becker, Michael M.

; APPLICANT: Majlessi, Mehrdad

; TITLE OF INVENTION: METHODS FOR DETECTING AND

; TITLE OF INVENTION: AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED

; TITLE OF INVENTION: OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gen-Probe Incorporated

; STREET: 10210 Genetic Center Drive

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

```

;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/893,300
;     FILING DATE:  15-JUL-1997
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  60/021,818
;     FILING DATE:  15-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Cappellari, Charles B
;     REGISTRATION NUMBER:  40,937
;     REFERENCE/DOCKET NUMBER:  CHE7B-P01A01
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  619-410-8927
;     TELEFAX:  619-410-8928
;     TELEX:
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-893-300-1

```

```

Query Match          100.0%;  Score 19;  DB 3;  Length 26;
Best Local Similarity 100.0%;  Pred. No. 0.31;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      1 TGCGGGACTTAACCCAACA 19
        |||
Db      7 TGCGGGACTTAACCCAACA 25

```

## RESULT 13

US-08-893-300-2/c

; Sequence 2, Application US/08893300

; Patent No. 6130038

; GENERAL INFORMATION:

; APPLICANT: Becker, Michael M.

; APPLICANT: Majlessi, Mehrdad

; TITLE OF INVENTION: METHODS FOR DETECTING AND

; TITLE OF INVENTION: AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED

; TITLE OF INVENTION: OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gen-Probe Incorporated

; STREET: 10210 Genetic Center Drive

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/893,300

; FILING DATE: 15-JUL-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/021,818

; FILING DATE: 15-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Cappellari, Charles B

; REGISTRATION NUMBER: 40,937

; REFERENCE/DOCKET NUMBER: CHE7B-P01A01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-410-8927

; TELEFAX: 619-410-8928

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

```

;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-893-300-2

```

Query Match 100.0%; Score 19; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGG ACT TTA ACC CAACA 19  
 |||||  
 Db 20 TGC GGG ACT TTA ACC CAACA 2

RESULT 14

```

US-09-736-151-4
; Sequence 4, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENUU, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-4

```

Query Match 100.0%; Score 19; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGG ACT TTA ACC CAACA 19  
          |||||  
Db 7 TGC GGG ACT TTA ACC CAACA 25

RESULT 15

```

US-09-736-151-5
; Sequence 5, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENUU, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA

```

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the  
; OTHER INFORMATION: phosphate between nucleotides at positions 16 and  
; OTHER INFORMATION: 17 is a thiophosphate  
US-09-736-151-5

Query Match 100.0%; Score 19; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 16

US-09-736-151-6

; Sequence 6, Application US/09736151  
; Patent No. 6902891  
; GENERAL INFORMATION:  
; APPLICANT: LAAYOUN, ALI  
; APPLICANT: MENU, LIONEL  
; APPLICANT: TORA, CHRISTELLE  
; APPLICANT: BANERJEE, ALOKE R.  
; APPLICANT: BECKER, MICHAEL M.  
; APPLICANT: BROWNE, KENNETH A.  
; APPLICANT: FRIEDENBERG, MATTHEW C.  
; APPLICANT: HAJJAR, FRED F.  
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID  
; FILE REFERENCE: 104959  
; CURRENT APPLICATION NUMBER: US/09/736,151  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/172,136  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the  
; OTHER INFORMATION: phosphate at the 3' end is a terminal  
; OTHER INFORMATION: thiophosphate  
US-09-736-151-6

Query Match 100.0%; Score 19; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 17

US-09-736-151-7

; Sequence 7, Application US/09736151  
; Patent No. 6902891  
; GENERAL INFORMATION:  
; APPLICANT: LAAYOUN, ALI  
; APPLICANT: MENU, LIONEL  
; APPLICANT: TORA, CHRISTELLE  
; APPLICANT: BANERJEE, ALOKE R.  
; APPLICANT: BECKER, MICHAEL M.  
; APPLICANT: BROWNE, KENNETH A.  
; APPLICANT: FRIEDENBERG, MATTHEW C.  
; APPLICANT: HAJJAR, FRED F.  
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID  
; FILE REFERENCE: 104959  
; CURRENT APPLICATION NUMBER: US/09/736,151  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/172,136  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the
; OTHER INFORMATION: phosphate between the two nucleotides at position
; OTHER INFORMATION: 16 and 17 is a thiophosphate
US-09-736-151-7
```

```
Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.31;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 TGCGGGACTTAACCCAACA 19
          :|||||||:|||||||
Db      7 UGCGGGACUUAACCCAACA 25
```

## RESULT 18

```
US-09-736-151-8
; Sequence 8, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer ; the
; OTHER INFORMATION: phosphate at the 3' end is a terminal
; OTHER INFORMATION: thiophosphate
US-09-736-151-8
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Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.31;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TGCGGGACTTAACCCAACA 19
          :|||||||:|||||||
Db      7 UGCGGGACUUAACCCAACA 25
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## RESULT 19

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US-09-736-151-9
; Sequence 9, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
; APPLICANT: LAAYOUN, ALI
; APPLICANT: MENOUE, LIONEL
; APPLICANT: TORA, CHRISTELLE
; APPLICANT: BANERJEE, ALOKE R.
; APPLICANT: BECKER, MICHAEL M.
; APPLICANT: BROWNE, KENNETH A.
; APPLICANT: FRIEDENBERG, MATTHEW C.
; APPLICANT: HAJJAR, FRED F.
; TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
; FILE REFERENCE: 104959
; CURRENT APPLICATION NUMBER: US/09/736,151
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; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/172,136
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-9
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Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.31;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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        :|||||||:|||||||
Db      7 UGCGGGACUUAACCCAACA 25
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RESULT 20

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US-09-523-237B-1/c
; Sequence 1, Application US/09523237B
; Patent No. 6903206
; GENERAL INFORMATION:
; APPLICANT: Becker, Michael M.
; APPLICANT: Majlessi, Mehrdad
; APPLICANT: Brentano, Steven T.
; TITLE OF INVENTION: Kits for Amplifying Nucleic Acid Sequences Using Modified
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: GP068-03.CN1
; CURRENT APPLICATION NUMBER: US/09/523,237B
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 08/893,300
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/021,818
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-523-237B-1
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Query Match          100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TCGGGGACTTAACCCAACA 19
        |||||||
Db      20 TCGGGGACTTAACCCAACA 2
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Search completed: July 26, 2006, 16:03:15  
Job time : 70.439 secs

SCORE 1.3 BuildDate: 12/06/2005

.

start

OM nucleic - nucleic search, using sw model

http://es/ScoreAccessWeb/GetItem.action?AppId=10743384&seqId=570248&ItemName=us... 7/31/06

c	3	19	100.0	19	2	AR478760	AR478760 Sequence
	4	19	100.0	21	2	AR452380	AR452380 Sequence
	5	19	100.0	21	2	AX201200	AX201200 Sequence
c	6	19	100.0	23	2	BD205810	BD205810 A method
c	7	19	100.0	23	2	AX010473	AX010473 Sequence
	8	19	100.0	25	2	AX463303	AX463303 Sequence
	9	19	100.0	26	2	AR112109	AR112109 Sequence
c	10	19	100.0	26	2	AR112110	AR112110 Sequence
	11	19	100.0	26	2	I93509	I93509 Sequence 5
c	12	19	100.0	26	2	I93510	I93510 Sequence 6
	13	19	100.0	26	2	I93515	I93515 Sequence 11
c	14	19	100.0	26	2	I93516	I93516 Sequence 12
	15	19	100.0	26	2	AR678434	AR678434 Sequence
	16	19	100.0	26	2	AR678435	AR678435 Sequence
	17	19	100.0	26	2	AR678436	AR678436 Sequence
	18	19	100.0	26	2	AR678437	AR678437 Sequence
	19	19	100.0	26	2	AR678438	AR678438 Sequence
	20	19	100.0	26	2	AR678439	AR678439 Sequence
c	21	19	100.0	26	2	AR680175	AR680175 Sequence
	22	19	100.0	26	2	AR680176	AR680176 Sequence
	23	19	100.0	26	2	AR680177	AR680177 Sequence
	24	19	100.0	26	2	AR680178	AR680178 Sequence
	25	19	100.0	26	2	AR680179	AR680179 Sequence
	26	19	100.0	26	2	AR680180	AR680180 Sequence
	27	19	100.0	26	2	AR680181	AR680181 Sequence
c	28	19	100.0	26	2	AR680182	AR680182 Sequence
c	29	19	100.0	26	2	AR680183	AR680183 Sequence
	30	19	100.0	26	2	AR680184	AR680184 Sequence
	31	19	100.0	26	2	AR680185	AR680185 Sequence
	32	19	100.0	26	2	AX166827	AX166827 Sequence
	33	19	100.0	26	2	AX166828	AX166828 Sequence
	34	19	100.0	26	2	AX166829	AX166829 Sequence
	35	19	100.0	26	2	AX166830	AX166830 Sequence
	36	19	100.0	26	2	AX166831	AX166831 Sequence
	37	19	100.0	26	2	AX166832	AX166832 Sequence
	38	19	100.0	26	2	AX463301	AX463301 Sequence
c	39	19	100.0	26	2	AX463302	AX463302 Sequence
c	40	19	100.0	51	2	CQ819522	CQ819522 Sequence
c	41	19	100.0	59	2	AR358840	AR358840 Sequence
c	42	19	100.0	59	2	AR540396	AR540396 Sequence
	43	17.4	91.6	33	2	BD140319	BD140319 Universal
c	44	17	89.5	23	2	BD205788	BD205788 A method
c	45	17	89.5	23	2	AX010451	AX010451 Sequence
c	46	14.4	75.8	60	2	CQ553680	CQ553680 Sequence
c	47	14	73.7	22	2	AR071559	AR071559 Sequence
c	48	14	73.7	22	2	I40288	I40288 Sequence 46
c	49	14	73.7	22	2	AR526803	AR526803 Sequence
	50	14	73.7	25	2	AR089513	AR089513 Sequence
	51	13.4	70.5	22	2	AR372759	AR372759 Sequence
	52	13.4	70.5	22	2	AX010413	AX010413 Sequence
	53	13.4	70.5	25	2	BD001703	BD001703 Compositi
	54	13.4	70.5	25	2	BD001716	BD001716 Method fo
	55	13.2	69.5	51	2	BD171631	BD171631 Method fo
	56	13.2	69.5	51	2	AR404984	AR404984 Sequence
	57	13.2	69.5	51	2	AX441330	AX441330 Sequence
c	58	13	68.4	13	2	CQ819524	CQ819524 Sequence
c	59	13	68.4	20	2	AX746436	AX746436 Sequence
	60	13	68.4	21	2	AR452382	AR452382 Sequence

## ALIGNMENTS

## RESULT 1

CQ818165

LOCUS CQ818165 19 bp DNA linear PAT 07-JUN-2004

DEFINITION Sequence 2 from Patent WO2004044247.

ACCESSION CQ818165

VERSION CQ818165.1 GI:48426957

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Chaubron,F., Martin-Minvielle,A.C. and Groulon,S.

TITLE One step real-time rt pcr kits for the universal detection of

organisms in industrial products  
 JOURNAL Patent: WO 2004044247-A 2 27-MAY-2004;  
 Genolife (FR)  
 FEATURES Location/Qualifiers  
   source 1..19  
           /organism="synthetic construct"  
           /mol\_type="unassigned DNA"  
           /db\_xref="taxon:32630"  
           /note="#Description of artificial sequence:  
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 Query Match 100.0%; Score 19; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGGGACTTAACCCAACA 19  
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 Db 1 TCGGGGACTTAACCCAACA 19

RESULT 2  
 AR478754  
 LOCUS AR478754 19 bp DNA linear PAT 14-MAY-2004  
 DEFINITION Sequence 2 from patent US 6699670.  
 ACCESSION AR478754  
 VERSION AR478754.1 GI:47237474  
 KEYWORDS .  
 SOURCE Unknown.  
   ORGANISM Unknown.  
           Unclassified.  
 REFERENCE 1 (bases 1 to 19)  
   AUTHORS Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.  
   TITLE Quantitative assay for the simultaneous detection and speciation of  
           bacterial infections  
   JOURNAL Patent: US 6699670-A 2 02-MAR-2004;  
           The Johns Hopkins University; Baltimore, MD  
 FEATURES Location/Qualifiers  
   source 1..19  
           /organism="unknown"  
           /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 100.0%; Score 19; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGGGACTTAACCCAACA 19  
       |||||  
 Db 1 TCGGGGACTTAACCCAACA 19

RESULT 3  
 AR478760/c  
 LOCUS AR478760 19 bp DNA linear PAT 14-MAY-2004  
 DEFINITION Sequence 8 from patent US 6699670.  
 ACCESSION AR478760  
 VERSION AR478760.1 GI:47237480  
 KEYWORDS .  
 SOURCE Unknown.  
   ORGANISM Unknown.  
           Unclassified.  
 REFERENCE 1 (bases 1 to 19)  
   AUTHORS Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.  
   TITLE Quantitative assay for the simultaneous detection and speciation of  
           bacterial infections  
   JOURNAL Patent: US 6699670-A 8 02-MAR-2004;  
           The Johns Hopkins University; Baltimore, MD  
 FEATURES Location/Qualifiers  
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           /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 100.0%; Score 19; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 19 TGCGGGACTTAACCCAACA 1

## RESULT 4

AR452380  
 LOCUS AR452380 21 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 25 from patent US 6677153.  
 ACCESSION AR452380  
 VERSION AR452380.1 GI:42684027  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Iversen, P.L.  
 TITLE Antisense antibacterial method and composition  
 JOURNAL Patent: US 6677153-A 25 13-JAN-2004;  
 AVI BioPharma, Inc.; Covallis, OR  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 2 TGCGGGACTTAACCCAACA 20

## RESULT 5

AX201200  
 LOCUS AX201200 21 bp DNA linear PAT 29-AUG-2001  
 DEFINITION Sequence 25 from Patent WO0142457.  
 ACCESSION AX201200  
 VERSION AX201200.1 GI:15390952  
 KEYWORDS .  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Iversen, P.L.  
 TITLE Antisense antibacterial method and composition  
 JOURNAL Patent: WO 0142457-A 25 14-JUN-2001;  
 Avi Biopharma, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="antisense oligomer"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 2 TGCGGGACTTAACCCAACA 20

## RESULT 6

BD205810/c  
 LOCUS BD205810 23 bp DNA linear PAT 17-JUL-2003  
 DEFINITION A method for detecting microorganisms in products.  
 ACCESSION BD205810  
 VERSION BD205810.1 GI:33015580  
 KEYWORDS JP 2002514439-A/52.

SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 23)  
 AUTHORS Gerbling,K.P., Lauter,F.R. and Grohmann,L.  
 TITLE A method for detecting microorganisms in products  
 JOURNAL Patent: JP 2002514439-A 52 21-MAY-2002;  
 BIOINSIDE GMBH

COMMENT OS Artificial Sequence  
 PN JP 2002514439-A/52  
 PD 21-MAY-2002  
 PF 10-MAY-1999 JP 2000548504  
 PR 12-MAY-1998 DE 198 22 108.8  
 PI KLAUS PETER GERBLING,FRANK ROMAN LAUTER,LUTZ GROHMANN PC  
 C12N15/09,C12Q1/68,C12N15/00  
 CC Description of Artificial Sequence: sonde  
 FH Key Location/Qualifiers  
 FT source 1..23  
 FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers  
 source 1..23  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
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 Db 20 TGC GGGACTTAACCCAACA 2

## RESULT 7

AX010473/c

LOCUS AX010473 23 bp DNA linear PAT 06-SEP-2000

DEFINITION Sequence 52 from Patent WO9958713.

ACCESSION AX010473

VERSION AX010473.1 GI:9997316

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Grohmann,L., Gerbling,K.P. and Lauter,F.R.

TITLE Method for detecting microorganisms in products

JOURNAL Patent: WO 9958713-A 52 18-NOV-1999;  
 GROHMANN LUTZ (DE); BIOINSIDE GMBH (DE); GERBLING KLAUS PETER (DE);  
 LAUTER FRANK ROMAN (DE)

FEATURES Location/Qualifiers

source 1..23  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
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## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
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Qy 1 TGC GGGACTTAACCCAACA 19  
 |||||  
 Db 20 TGC GGGACTTAACCCAACA 2

## RESULT 8

AX463303

LOCUS AX463303 25 bp DNA linear PAT 15-JUL-2002

DEFINITION Sequence 3 from Patent WO0248404.

ACCESSION AX463303

VERSION AX463303.1 GI:21886254

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Becker,M.M.

TITLE Method and kit for enhancing the association rates of polynucleotides

JOURNAL Patent: WO 0248404-A 3 20-JUN-2002;  
Gen-Probe Incorporated (US)

FEATURES Location/Qualifiers  
source 1. .25  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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Db 6 TGCGGGACTTAACCCAACA 24

## RESULT 9

AR112109

LOCUS AR112109 26 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 1 from patent US 6130038.

ACCESSION AR112109

VERSION AR112109.1 GI:14092009

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Becker,M.M., Majlessi,M. and Brentano,S.T.

TITLE Method for amplifying target nucleic acids using modified primers

JOURNAL Patent: US 6130038-A 1 10-OCT-2000;

FEATURES Location/Qualifiers  
source 1. .26  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
|||||  
Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 10

AR112110/c

LOCUS AR112110 26 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 2 from patent US 6130038.

ACCESSION AR112110

VERSION AR112110.1 GI:14092010

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Becker,M.M., Majlessi,M. and Brentano,S.T.

TITLE Method for amplifying target nucleic acids using modified primers

JOURNAL Patent: US 6130038-A 2 10-OCT-2000;

FEATURES Location/Qualifiers  
source 1. .26  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
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 Db 20 TGC GGGACTTAACCCAACA 2

## RESULT 11

I93509

LOCUS I93509 26 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 5 from patent US 5731148.

ACCESSION I93509

VERSION I93509.1 GI:3937979

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Becker,M. and Nelson,N.C.

TITLE Adduct protection assay

JOURNAL Patent: US 5731148-A 5 24-MAR-1998;

FEATURES Location/Qualifiers

source 1. .26

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.2e+05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
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 Db 7 TGC GGGACTTAACCCAACA 25

## RESULT 12

I93510/c

LOCUS I93510 26 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 6 from patent US 5731148.

ACCESSION I93510

VERSION I93510.1 GI:3937980

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Becker,M. and Nelson,N.C.

TITLE Adduct protection assay

JOURNAL Patent: US 5731148-A 6 24-MAR-1998;

FEATURES Location/Qualifiers

source 1. .26

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.2e+05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
 |||||  
 Db 20 TGC GGGACTTAACCCAACA 2

## RESULT 13

I93515

LOCUS I93515 26 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 11 from patent US 5731148.

ACCESSION I93515

VERSION I93515.1 GI:3937985

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Becker,M. and Nelson,N.C.

TITLE Adduct protection assay  
 JOURNAL Patent: US 5731148-A 11 24-MAR-1998;  
 FEATURES Location/Qualifiers  
   source 1. .26  
           /organism="unknown"  
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## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
    |||||  
 Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 14

I93516/c  
 LOCUS I93516 26 bp DNA linear PAT 01-DEC-1998  
 DEFINITION Sequence 12 from patent US 5731148.  
 ACCESSION I93516  
 VERSION I93516.1 GI:3937986  
 KEYWORDS .  
 SOURCE Unknown.  
   ORGANISM Unknown.  
           Unclassified.  
 REFERENCE 1 (bases 1 to 26)  
   AUTHORS Becker,M. and Nelson,N.C.  
   TITLE Adduct protection assay  
   JOURNAL Patent: US 5731148-A 12 24-MAR-1998;  
 FEATURES Location/Qualifiers  
   source 1. .26  
           /organism="unknown"  
           /mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
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 Db 20 TGCGGGACTTAACCCAACA 2

## RESULT 15

AR678434  
 LOCUS AR678434 26 bp DNA linear PAT 13-JUN-2005  
 DEFINITION Sequence 4 from patent US 6902891.  
 ACCESSION AR678434  
 VERSION AR678434.1 GI:67619142  
 KEYWORDS .  
 SOURCE Unknown.  
   ORGANISM Unknown.  
           Unclassified.  
 REFERENCE 1 (bases 1 to 26)  
   AUTHORS Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,  
           Browne,K.A., Friedenber,M.C. and Hajjar,F.F.  
   TITLE Process for labeling a nucleic acid  
   JOURNAL Patent: US 6902891-A 4 07-JUN-2005;  
           Bio Merieux and Gen-Probe Incorporated; Marcy 1' Etoile;  
           FRX;  
 FEATURES Location/Qualifiers  
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           /mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
    |||||  
 Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 16

AR678435

LOCUS AR678435 26 bp DNA linear PAT 13-JUN-2005

DEFINITION Sequence 5 from patent US 6902891.

ACCESSION AR678435

VERSION AR678435.1 GI:67619143

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,  
Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.

TITLE Process for labeling a nucleic acid

JOURNAL Patent: US 6902891-A 5 07-JUN-2005;  
Bio Merieux and Gen-Probe Incorporated; Marcy 1' Etoile;  
FRX;

FEATURES Location/Qualifiers

source 1..26  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.2e+05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19

|||||

Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 17

AR678436

LOCUS AR678436 26 bp DNA linear PAT 13-JUN-2005

DEFINITION Sequence 6 from patent US 6902891.

ACCESSION AR678436

VERSION AR678436.1 GI:67619144

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 26)

AUTHORS Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,  
Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.

TITLE Process for labeling a nucleic acid

JOURNAL Patent: US 6902891-A 6 07-JUN-2005;  
Bio Merieux and Gen-Probe Incorporated; Marcy 1' Etoile;  
FRX;

FEATURES Location/Qualifiers

source 1..26  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 7.2e+05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19

|||||

Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 18

AR678437

LOCUS AR678437 26 bp RNA linear PAT 13-JUN-2005

DEFINITION Sequence 7 from patent US 6902891.

ACCESSION AR678437

VERSION AR678437.1 GI:67619147

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,  
 Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.  
 TITLE Process for labeling a nucleic acid  
 JOURNAL Patent: US 6902891-A 7 07-JUN-2005;  
 Bio Merieux and Gen-Probe Incorporated; Marcy 1' Etoile;  
 FRX;

FEATURES Location/Qualifiers  
 source 1..26  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 7 TGCGGGACTTAACCCAACA 25

RESULT 19  
 AR678438  
 LOCUS AR678438 26 bp RNA linear PAT 13-JUN-2005  
 DEFINITION Sequence 8 from patent US 6902891.  
 ACCESSION AR678438  
 VERSION AR678438.1 GI:67619148  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,  
 Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.  
 TITLE Process for labeling a nucleic acid  
 JOURNAL Patent: US 6902891-A 8 07-JUN-2005;  
 Bio Merieux and Gen-Probe Incorporated; Marcy 1' Etoile;  
 FRX;

FEATURES Location/Qualifiers  
 source 1..26  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 7 TGCGGGACTTAACCCAACA 25

RESULT 20  
 AR678439  
 LOCUS AR678439 26 bp RNA linear PAT 13-JUN-2005  
 DEFINITION Sequence 9 from patent US 6902891.  
 ACCESSION AR678439  
 VERSION AR678439.1 GI:67619149  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,  
 Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.  
 TITLE Process for labeling a nucleic acid  
 JOURNAL Patent: US 6902891-A 9 07-JUN-2005;  
 Bio Merieux and Gen-Probe Incorporated; Marcy 1' Etoile;  
 FRX;

FEATURES Location/Qualifiers  
 source 1..26  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
 |||||  
 Db 7 TGC GGGACTTAACCCAACA 25

Search completed: July 26, 2006, 18:08:14  
 Job time : 1247.2 secs

SCORE 1.3 BuildDate: 12/06/2005

# SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-1.szm60.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 15:45:05 ; Search time 246.293 Seconds  
(without alignments)  
622.793 Million cell updates/sec

Title: US-10-743-384-1  
Perfect score: 22  
Sequence: 1 tggagcatgtggtttaattcga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5397982

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 60 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	22	100.0	22	6 ABS71588	Abs71588 Bacterial
2	22	100.0	22	6 ABS71584	Abs71584 Forward p

	3	22	100.0	22	12	ADO15325	Ado15325 PCR prime
	4	22	100.0	52	3	AAA14443	Aaa14443 Escherich
	5	22	100.0	52	5	AAC63206	Aac63206 16S rRNA
c	6	22	100.0	52	5	AAC63204	Aac63204 Capture p
c	7	21	95.5	22	2	AAX60967	Aax60967 Donor pro
	8	20.2	91.8	22	12	ADO15329	Ado15329 PCR prime
c	9	20	90.9	24	10	ABZ23211	Abz23211 PCR prime
	10	18.8	85.5	20	2	AAV51392	Aav51392 Microbial
	11	18	81.8	21	13	ADS15239	Ads15239 H.pylori
	12	18	81.8	34	4	AAH28414	Aah28414 PCR prime
	13	17.8	80.9	30	14	AED50849	Aed50849 16S rRNA
	14	17.8	80.9	30	14	AED50847	Aed50847 16S rRNA
	15	17.8	80.9	30	14	AED50848	Aed50848 16S rRNA
	16	17.8	80.9	30	14	AED50850	Aed50850 16S rRNA
c	17	17.2	78.2	42	1	AAN92213	Aan92213 Helper ol
c	18	17.2	78.2	42	1	AAN92920	Aan92920 Helper ol
c	19	17.2	78.2	42	5	AAF23125	Aaf23125 N. gonorr
	20	17.2	78.2	46	2	AAQ85201	Aaq85201 Ureaplasma
	21	17.2	78.2	46	2	AAQ85200	Aaq85200 Ureaplasma
c	22	17.2	78.2	46	2	AAQ85163	Aaq85163 Ureaplasma
c	23	17.2	78.2	46	2	AAQ85199	Aaq85199 Ureaplasma
c	24	17	77.3	19	12	ADO18316	Ado18316 Analytica
c	25	17	77.3	19	12	ADO18550	Ado18550 Analytica
c	26	17	77.3	19	12	ADO18518	Ado18518 Analytica
c	27	17	77.3	19	12	ADO18336	Ado18336 Analytica
c	28	16.2	73.6	24	1	AAN90467	Aan90467 Escherich
c	29	16.2	73.6	24	2	AAQ10475	Aaq10475 Probe UP2
c	30	16	72.7	16	2	AAT10133	Aat10133 Primer SA
	31	16	72.7	21	13	ADU74086	Adu74086 Bacillus
c	32	16	72.7	40	2	AAT10136	Aat10136 Modified
c	33	16	72.7	40	2	AAX60966	Aax60966 Beacon pr
	34	15.6	70.9	57	12	ADO85479	Ado85479 Fungal 18
c	35	15.4	70.0	19	12	ADO18736	Ado18736 Analytica
c	36	15.4	70.0	19	12	ADO18473	Ado18473 Analytica
	37	15.4	70.0	40	3	AAC64803	Aac64803 Novel str
	38	15.4	70.0	40	3	AAC63124	Aac63124 Novel str
	39	15.4	70.0	40	3	AAC65214	Aac65214 Allele-sp
	40	15.4	70.0	40	3	AAC65147	Aac65147 Novel str
	41	15.4	70.0	40	5	AAC63605	Aac63605 Bacterial
	42	15.4	70.0	40	5	AAC64865	Aac64865 Novel str
	43	15	68.2	24	3	AAA14444	Aaa14444 Tether ol
	44	15	68.2	24	5	AAC63205	Aac63205 Fluoresce
	45	15	68.2	38	8	ACC97168	Acc97168 Consensus
c	46	14.8	67.3	31	3	AAA29977	Aaa29977 PCR prime
c	47	14.8	67.3	50	6	ABZ05357	Abz05357 Human leu
	48	14.6	66.4	25	13	ADR56581	Adr56581 Drug ther
c	49	14.6	66.4	47	10	ADF16934	Adf16934 Human alb
c	50	14.6	66.4	47	10	ADH22002	Adh22002 Human PYY
c	51	14.4	65.5	18	14	AEC09679	Aec09679 Primer 16
	52	14.4	65.5	50	6	ABZ03588	Abz03588 Human leu
c	53	14.2	64.5	21	14	ACL41182	Ac141182 C20orf103
c	54	14.2	64.5	21	14	ACL41183	Ac141183 C20orf103
	55	14.2	64.5	21	14	ACL41184	Ac141184 C20orf103
c	56	14.2	64.5	23	14	AEB16517	Aeb16517 Human SLC
	57	14.2	64.5	29	14	AEB16504	Aeb16504 Human SLC
c	58	14.2	64.5	30	14	ADZ71240	Adz71240 Human pla
c	59	14.2	64.5	31	14	ADZ71218	Adz71218 Human pla
	60	14.2	64.5	33	6	AAL38408	Aal38408 Beta-gala

## ALIGNMENTS

## RESULT 1

ABS71588

ID ABS71588 standard; DNA; 22 BP.

XX

AC ABS71588;

XX

DT 28-NOV-2002 (first entry)

XX

DE Bacterial 16s RNA fragment for primer design #1.

XX

KW Eubacteria; species detection; speciation; 16s RNA; ds.

XX

OS Staphylococcus aureus.

XX  
 PN WO200270728-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US006050.  
 XX  
 PR 01-MAR-2001; 2001US-0272642P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Rothman RE, Yang S, Lin S, Kelen GD;  
 XX  
 DR WPI; 2002-698755/75.  
 XX  
 PT Detecting and determining species source of eubacterial DNA in a sample,  
 PT comprises amplifying template DNA in the sample using a real-time  
 PT polymerase chain reaction with the use of primers and at least two  
 PT fluorogenic probes.  
 XX  
 PS Disclosure; Fig 5; 39pp; English.  
 XX  
 CC The invention describes a method of detecting and determining species  
 CC source of eubacterial DNA in a sample. The method comprises amplifying  
 CC template DNA in the sample using a real-time polymerase chain reaction (R  
 CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at  
 CC least two fluorogenic probes. The methods are useful in detecting and  
 CC determining species source of eubacterial DNA in a sample. The present  
 CC method allows for highly sensitive detection of any eubacterial species  
 CC with simultaneous speciation. It eliminates false positive results in  
 CC detecting bacterial infections. This sequence represents a bacterial 16s  
 CC RNA sequence used to create primers for use in the eubacterial detection  
 CC method of the invention  
 XX  
 SQ Sequence 22 BP; 5 A; 2 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.93;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCGA 22  
 |||||  
 Db 1 TGGAGCATGTGGTTTAATTCGA 22

## RESULT 2

ABS71584

ID ABS71584 standard; DNA; 22 BP.

XX

AC ABS71584;

XX

DT 28-NOV-2002 (first entry)

XX

DE Forward primer for detecting bacterial infection P890F.

XX

KW Eubacteria; species detection; speciation; 16s RNA; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200270728-A2.

XX

PD 12-SEP-2002.

XX

PF 01-MAR-2002; 2002WO-US006050.

XX

PR 01-MAR-2001; 2001US-0272642P.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Rothman RE, Yang S, Lin S, Kelen GD;

XX

DR WPI; 2002-698755/75.

XX

PT Detecting and determining species source of eubacterial DNA in a sample,

PT comprises amplifying template DNA in the sample using a real-time

PT polymerase chain reaction with the use of primers and at least two

PT fluorogenic probes.  
 XX  
 PS Claim 12; Page 11; 39pp; English.  
 XX  
 CC The invention describes a method of detecting and determining species  
 CC source of eubacterial DNA in a sample. The method comprises amplifying  
 CC template DNA in the sample using a real-time polymerase chain reaction (R  
 CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at  
 CC least two fluorogenic probes. The methods are useful in detecting and  
 CC determining species source of eubacterial DNA in a sample. The present  
 CC method allows for highly sensitive detection of any eubacterial species  
 CC with simultaneous speciation. It eliminates false positive results in  
 CC detecting bacterial infections. This sequence represents a primer  
 CC designed using 16s RNA sequences and used in the eubacterial detection  
 CC method of the invention  
 XX  
 SQ Sequence 22 BP; 5 A; 2 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.93;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCGA 22  
 |||||  
 Db 1 TGGAGCATGTGGTTTAATTCGA 22

## RESULT 3

ADO15325

ID ADO15325 standard; DNA; 22 BP.

XX

AC ADO15325;

XX

DT 12-AUG-2004 (first entry)

XX

DE PCR primer used for one-step real-time RT-PCR detection SeqID 1.

XX

KW one step real-time RT-PCR; pharmaceutical; cosmetic; bacteria;

KW fungus-yeast; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO2004044247-A2.

XX

PD 27-MAY-2004.

XX

PF 03-NOV-2003; 2003WO-IB005312.

XX

PR 12-NOV-2002; 2002US-0425327P.

XX

PA (GENO-) GENOLIFE.

XX

PI Chaubron F, Martin-Minvielle AC, Groulon S;

XX

DR WPI; 2004-411742/38.

XX

PT Determining presence of bacteria or fungus-yeast RNA in sample involves

PT carrying out reverse transcriptase-PCR reaction of fungus-yeast RNA and

PT treating amplified DNA with probes which hybridize to amplified DNA.

XX

PS Claim 1; SEQ ID NO 1; 31pp; English.

XX

CC This invention relates to a novel method for one step real-time RT-PCR  
 CC kits useful for the detection of microorganisms occurring within  
 CC industrial products such as pharmaceuticals, cosmetic and non-clinical  
 CC samples. Specifically, it refers to determining the presence of bacteria  
 CC or fungus-yeast RNA in a sample suspected of containing such  
 CC contaminants. The present invention describes oligonucleotide primers and  
 CC probes that are natural nucleic acid or peptide nucleic acid (PNA)  
 CC molecules that can hybridize to the target nucleic acid (DNA and RNA).  
 CC Accordingly, the method enables rapid and simultaneous detection and  
 CC quantification of RNA from bacteria and fungus-yeast in either sterile or  
 CC non-sterile products in less than 24 hours. Furthermore, the one step  
 CC process reduces the risk of environmental contamination that could occur  
 CC when the reaction tubes are opened during the PCR procedure. This  
 CC oligonucleotide sequence is a PCR primer used in one-step real time RT-

CC PCR to amplify bacteria and fungus-yeast RNA, given in an exemplification  
CC of the invention.  
XX  
SQ Sequence 22 BP; 5 A; 2 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCGA 22  
|||||  
Db 1 TGGAGCATGTGGTTTAATTCGA 22

## RESULT 4

AAA14443

ID AAA14443 standard; DNA; 52 BP.

XX

AC AAA14443;

XX

DT 21-AUG-2000 (first entry)

XX

DE Escherichia coli 16S rRNA gene fragment template.

XX

KW Reverse displacement assay; nucleic acid detection; hybridisation;

KW 16S ribosomal RNA gene; ss.

XX

OS Escherichia coli.

XX

PN WO200020643-A1.

XX

PD 13-APR-2000.

XX

PF 04-OCT-1999; 99WO-US023035.

XX

PR 05-OCT-1998; 98US-0103075P.

XX

PA (MOSA-) MOSAIC TECHNOLOGIES.

XX

PI Abrams ES, Hammond PW;

XX

DR WPI; 2000-303807/26.

XX

PT Method for detecting the presence of a target nucleic acid sequence in a  
PT test sample.

XX

PS Example; Page 17; 30pp; English.

XX

CC The invention relates to a novel method for detecting the presence of a  
CC target nucleic acid sequence in a test sample. The method comprises  
CC forming a probe-tether complex and introducing a test sample into a  
CC solution containing the complex under conditions suitable for  
CC hybridisation between the probe and the target. A probe-target complex is  
CC formed, and the presence of the target nucleic acid sequence is detected  
CC in the test sample. The probe is complementary to the target sequence,  
CC while the tether is complementary to at least one subsequence of the  
CC probe. The probe-complex is contains at least one double stranded segment  
CC and one single stranded segment. Introduction of the target nucleic acid  
CC sequence displaces the tether sequence from the probe. If the probe  
CC and/or the tether contain a detectable label (e.g., a fluorophore), the  
CC reverse displacement can be detected by an alteration in the signal  
CC produced. Saturation of the tether nucleic acid with labelled probe is  
CC not required in this method, unlike prior art methods. Because the tether  
CC nucleic acid is not complementary to the target nucleic acid, uncomplexed  
CC tether nucleic acid will not hybridise with the target, and therefore  
CC does not compete with target nucleic acid for hybridisation with probe  
CC nucleic acids. In the exemplification of the invention, an  
CC oligonucleotide (AAA14443) corresponding to a portion of the Escherichia  
CC coli 16S ribosomal RNA gene was detected according to the method of the  
CC invention using probe AAA14445 and tether oligonucleotide AAA14444. The  
CC present sequence represents the Escherichia coli 16S ribosomal RNA gene  
CC fragment used as the target nucleic acid

XX

SQ Sequence 52 BP; 15 A; 12 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 52;

Best Local Similarity 100.0%; Pred. No. 1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
|||||  
Db 10 TGGAGCATGTGGTTTAATTCGA 31

## RESULT 5

AAC63206

ID AAC63206 standard; DNA; 52 BP.

XX

AC AAC63206;

XX

DT 06-FEB-2001 (first entry)

XX

DE 16S rRNA fragment.

XX

KW Microorganism detection; 16S rRNA; ss.

XX

OS Escherichia coli.

XX

PN WO200060120-A2.

XX

PD 12-OCT-2000.

XX

PF 31-MAR-2000; 2000WO-US008773.

XX

PR 02-APR-1999; 99US-00286091.

XX

PA (MOSA-) MOSAIC TECHNOLOGIES.

XX

PI Boles TC;

XX

DR WPI; 2001-015657/02.

XX

PT Detecting presence or absence of microbial target molecules  
PT electrophoretically, by using capture probes immobilized to  
PT electrophoretic matrix, that specifically bind to target molecule in test  
PT sample.

XX

PS Claim 27; Page 35; 6lpp; English.

XX

CC The present invention relates to a method for detecting the presence or  
CC absence of a microorganism in a biological sample by electrophoresis. The  
CC method of the present invention comprises detecting the presence or  
CC absence of microbiological target molecules in a test sample using  
CC capture probes, immobilised to an electrophoretic medium, which  
CC specifically bind to or are bound by the specific microbiological target  
CC molecules. The method of the present invention is useful for identifying  
CC bacteria Serratia marcescens, Staphylococcus epidermidis, Staphylococcus  
CC aureus, Escherichia coli, Bacillus cereus, Enterobacter cloacae,  
CC Streptococcus pyogenes, Staphylococcus warneri, Streptococcus (alpha-  
CC hemolytic), Streptococcus mitis, Salmonella, Serratia liquifaciens,  
CC Klebsiella, Propionibacterium acnes, Yersinia enterocolitica, Pseudomonas  
CC fluorescens, Pseudomonas putida in a biological sample. The present  
CC sequence is a DNA corresponding to the 16S rRNA sequence of E. coli. This  
CC sequence was used as a microbiological target molecule in the method of  
CC the present invention

XX

SQ Sequence 52 BP; 15 A; 12 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
|||||  
Db 10 TGGAGCATGTGGTTTAATTCGA 31

## RESULT 6

AAC63204/c

ID AAC63204 standard; DNA; 52 BP.

XX

AC AAC63204;

XX  
 DT 06-FEB-2001 (first entry)  
 XX  
 DE Capture probe #2 used for detecting microorganisms.  
 XX  
 KW Microorganism detection; capture probe; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN WO200060120-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 31-MAR-2000; 2000WO-US008773.  
 XX  
 PR 02-APR-1999; 99US-00286091.  
 XX  
 PA (MOSA-) MOSAIC TECHNOLOGIES.  
 XX  
 PI Boles TC;  
 XX  
 DR WPI; 2001-015657/02.  
 XX  
 PT Detecting presence or absence of microbial target molecules  
 PT electrophoretically, by using capture probes immobilized to  
 PT electrophoretic matrix, that specifically bind to target molecule in test  
 PT sample.  
 XX  
 PS Claim 25; Page 34; 61pp; English.  
 XX  
 CC The present invention relates to a method for detecting the presence or  
 CC absence of a microorganism in a biological sample by electrophoresis. The  
 CC method of the present invention comprises detecting the presence or  
 CC absence of microbiological target molecules in a test sample using  
 CC capture probes, immobilised to an electrophoretic medium, which  
 CC specifically bind to or are bound by the specific microbiological target  
 CC molecules. The method of the present invention is useful for identifying  
 CC bacteria Serratia marcescens, Staphylococcus epidermidis, Staphylococcus  
 CC aureus, Escherichia coli, Bacillus cereus, Enterobacter cloacae,  
 CC Streptococcus pyogenes, Staphylococcus warneri, Streptococcus (alpha-  
 CC hemolytic), Streptococcus mitis, Salmonella, Serratia liquifaciens,  
 CC Klebsiella, Propionibacterium acnes, Yersinia enterocolitica, Pseudomonas  
 CC fluorescens, Pseudomonas putida in a biological sample. The present  
 CC sequence is a capture probe used in the method of the present invention  
 XX  
 SQ Sequence 52 BP; 11 A; 14 C; 12 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
 |||||  
 Db 43 TGGAGCATGTGGTTTAATTCGA 22

## RESULT 7

AAX60967/c

ID AAX60967 standard; DNA; 22 BP.

XX

AC AAX60967;

XX

DT 03-SEP-1999 (first entry)

XX

DE Donor probe hybridising to a conserved eubacterial 16S rRNA.

XX

KW Nucleic acid detection; target; protein detection; pathogenic microbe;

KW eubacteria; human immune deficiency virus; blood contamination;

KW hybridisation; probe; ss.

XX

OS Synthetic.

XX

PN WO9926724-A2.

XX

PD 03-JUN-1999.

XX

PF 25-NOV-1998; 98WO-US024918.  
 XX  
 PR 25-NOV-1997; 97US-0066508P.  
 XX  
 PA (MOSA-) MOSAIC TECHNOLOGIES.  
 XX  
 PI Muir AR, Boles TC, Adams CP;  
 XX  
 DR WPI; 1999-385182/32.  
 XX  
 PT Device for detecting target molecule or microbe.  
 XX  
 PS Example 11; Page 78; 124pp; English.  
 XX  
 CC The invention describes a device for detecting presence of a target  
 CC molecule in a biological sample. The device comprises a receptacle  
 CC housing at least one chamber, having at least one compartment containing  
 CC one or more reagents for detecting the target. Optionally the device is  
 CC combined with, and optionally removable from, a collection device. The  
 CC devices are used to detect specific nucleic acids (RNA or DNA), proteins,  
 CC polypeptides, or a very wide range of pathogenic microbes (bacteria,  
 CC viruses, fungi or parasites), particularly eubacteria or human immune  
 CC deficiency virus. Especially the method is used to detect contamination  
 CC of donated blood. The devices are efficient, easy to use and provide  
 CC results rapidly  
 XX  
 SQ Sequence 22 BP; 8 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
  
 Query Match 95.5%; Score 21; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCG 21  
 |||||  
 Db 21 TGGAGCATGTGGTTTAATTCG 1

## RESULT 8

ADO15329

ID ADO15329 standard; DNA; 22 BP.

XX

AC ADO15329;

XX

DT 12-AUG-2004 (first entry)

XX

DE PCR primer used for one-step real-time RT-PCR detection SeqID 5.

XX

KW one step real-time RT-PCR; pharmaceutical; cosmetic; bacteria;

KW fungus-yeast; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO2004044247-A2.

XX

PD 27-MAY-2004.

XX

PF 03-NOV-2003; 2003WO-IB005312.

XX

PR 12-NOV-2002; 2002US-0425327P.

XX

PA (GENO-) GENOLIFE.

XX

PI Chaubron F, Martin-Minvielle AC, Groulon S;

XX

DR WPI; 2004-411742/38.

XX

PT Determining presence of bacteria or fungus-yeast RNA in sample involves

PT carrying out reverse transcriptase-PCR reaction of fungus-yeast RNA and

PT treating amplified DNA with probes which hybridize to amplified DNA.

XX

PS Claim 1; SEQ ID NO 5; 31pp; English.

XX

CC This invention relates to a novel method for one step real-time RT-PCR

CC kits useful for the detection of microorganisms occurring within

CC industrial products such as pharmaceuticals, cosmetic and non-clinical

CC samples. Specifically, it refers to determining the presence of bacteria

## RESULT 3

US-09-411-777A-1

; Sequence 1, Application US/09411777A

; Patent No. 6238927

; GENERAL INFORMATION:

; APPLICANT: Abrams, Ezra S.

; APPLICANT: Hammond, Philip W.

; TITLE OF INVENTION: Reverse Displacement Assay for Detection

; TITLE OF INVENTION: of Nucleic Acid Sequences

; FILE REFERENCE: MST98-03pA

; CURRENT APPLICATION NUMBER: US/09/411,777A

; CURRENT FILING DATE: 1999-10-04

; PRIOR APPLICATION NUMBER: 60/103,075

; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 52

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: target oligonucleotide

US-09-411-777A-1

Query Match 100.0%; Score 22; DB 3; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCGA 22

|||||

Db 10 TGGAGCATGTGGTTTAATTCGA 31

# SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384- 1.szm60.rge.

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 15:49:16 ; Search time 1441.8 Seconds  
(without alignments)  
975.751 Million cell updates/sec

Title: US-10-743-384-1  
Perfect score: 22  
Sequence: 1 tggagcatgtggtttaattcga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2455354

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 60 summaries

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- 2: gb\_pat:\*
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- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	22	100.0	22	2	CQ818164	CQ818164 Sequence
2	22	100.0	22	2	AR478753	AR478753 Sequence

3	22	100.0	22	2	AR478757	AR478757 Sequence
4	22	100.0	52	2	AR154667	AR154667 Sequence
c 5	21	95.5	22	2	AR159998	AR159998 Sequence
6	20.4	92.7	22	2	AR478761	AR478761 Sequence
7	20.2	91.8	22	2	CQ818168	CQ818168 Sequence
c 8	20	90.9	24	2	AX622955	AX622955 Sequence
9	20	90.9	25	2	AR089512	AR089512 Sequence
c 10	20	90.9	30	2	CS246054	CS246054 Sequence
11	18.8	85.5	20	2	E16621	E16621 PCR primer
c 12	17.2	78.2	46	2	AR104016	AR104016 Sequence
c 13	17.2	78.2	46	2	AR104091	AR104091 Sequence
14	17.2	78.2	46	2	AR104092	AR104092 Sequence
15	17.2	78.2	46	2	AR104093	AR104093 Sequence
c 16	17	77.3	19	2	CQ801775	CQ801775 Sequence
c 17	17	77.3	19	2	CQ801795	CQ801795 Sequence
c 18	16	72.7	41	2	AR159997	AR159997 Sequence
19	15.6	70.9	57	2	CQ819526	CQ819526 Sequence
c 20	15.4	70.0	19	2	CQ801932	CQ801932 Sequence
21	15.4	70.0	40	2	AR154163	AR154163 Sequence
22	15.4	70.0	40	2	AR175490	AR175490 Sequence
23	15.4	70.0	40	2	AR179265	AR179265 Sequence
24	15.4	70.0	40	2	BD190448	BD190448 AMPLIFICA
25	15.4	70.0	40	2	BD249373	BD249373 Electroni
26	15.4	70.0	40	2	AR352372	AR352372 Sequence
27	15.4	70.0	40	2	AR642735	AR642735 Sequence
28	15	68.2	24	2	AR154668	AR154668 Sequence
c 29	14.8	67.3	31	2	BD227690	BD227690 Expressio
c 30	14.8	67.3	31	2	AR281980	AR281980 Sequence
c 31	14.8	67.3	31	2	AR585402	AR585402 Sequence
c 32	14.8	67.3	50	2	AR685919	AR685919 Sequence
33	14.6	66.4	25	2	CQ865299	CQ865299 Sequence
c 34	14.6	66.4	47	2	DD180156	DD180156 Albumin F
35	14.4	65.5	50	2	AR684150	AR684150 Sequence
36	14.2	64.5	33	2	AX402424	AX402424 Sequence
c 37	14.2	64.5	51	2	CQ002165	CQ002165 Sequence
38	14.2	64.5	60	2	CQ537315	CQ537315 Sequence
39	13.8	62.7	50	2	AR683288	AR683288 Sequence
c 40	13.6	61.8	21	2	AR299176	AR299176 Sequence
41	13.6	61.8	24	2	AX665422	AX665422 Sequence
c 42	13.6	61.8	25	2	AX287101	AX287101 Sequence
c 43	13.6	61.8	28	2	CS059695	CS059695 Sequence
c 44	13.6	61.8	28	2	CS059696	CS059696 Sequence
c 45	13.6	61.8	30	2	AR308587	AR308587 Sequence
46	13.6	61.8	42	2	AR076833	AR076833 Sequence
47	13.6	61.8	42	2	BD014055	BD014055 Compositi
48	13.6	61.8	42	2	AR218141	AR218141 Sequence
49	13.6	61.8	42	2	AR634642	AR634642 Sequence.
50	13.6	61.8	47	2	AR288639	AR288639 Sequence
c 51	13.6	61.8	58	10	MLMGZ5	K03105 Gazdar muri
52	13.4	60.9	17	2	AX216228	AX216228 Sequence
53	13.4	60.9	17	2	AX216765	AX216765 Sequence
54	13.4	60.9	18	2	AX926901	AX926901 Sequence
55	13.4	60.9	21	2	CS068849	CS068849 Sequence
56	13.4	60.9	21	2	CS069059	CS069059 Sequence
c 57	13.4	60.9	46	2	AR032484	AR032484 Sequence
c 58	13.4	60.9	46	2	I29224	I29224 Sequence 96
c 59	13.4	60.9	46	2	AR209148	AR209148 Sequence
c 60	13.4	60.9	46	2	I90898	I90898 Sequence 96

## ALIGNMENTS

## RESULT 1

CQ818164

LOCUS CQ818164 22 bp DNA linear PAT 07-JUN-2004

DEFINITION Sequence 1 from Patent WO2004044247.

ACCESSION CQ818164

VERSION CQ818164.1 GI:48426956

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Chaubron,F., Martin-Minvielle,A.C. and Groulon,S.

TITLE One step real-time rt pcr kits for the universal detection of

organisms in industrial products  
 JOURNAL Patent: WO 2004044247-A 1 27-MAY-2004;  
 Genolife (FR)  
 FEATURES Location/Qualifiers  
   source 1. .22  
           /organism="synthetic construct"  
           /mol\_type="unassigned DNA"  
           /db\_xref="taxon:32630"  
           /note="#Description of artificial sequence:  
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 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
       |||||  
 Db 1 TGGAGCATGTGGTTTAATTCGA 22

RESULT 2  
 AR478753  
 LOCUS AR478753 22 bp DNA linear PAT 14-MAY-2004  
 DEFINITION Sequence 1 from patent US 6699670.  
 ACCESSION AR478753  
 VERSION AR478753.1 GI:47237473  
 KEYWORDS .  
 SOURCE Unknown.  
   ORGANISM Unknown.  
           Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
   AUTHORS Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.  
   TITLE Quantitative assay for the simultaneous detection and speciation of  
           bacterial infections  
   JOURNAL Patent: US 6699670-A 1 02-MAR-2004;  
           The Johns Hopkins University; Baltimore, MD  
 FEATURES Location/Qualifiers  
   source 1. .22  
           /organism="unknown"  
           /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 100.0%; Score 22; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
       |||||  
 Db 1 TGGAGCATGTGGTTTAATTCGA 22

RESULT 3  
 AR478757  
 LOCUS AR478757 22 bp DNA linear PAT 14-MAY-2004  
 DEFINITION Sequence 5 from patent US 6699670.  
 ACCESSION AR478757  
 VERSION AR478757.1 GI:47237477  
 KEYWORDS .  
 SOURCE Unknown.  
   ORGANISM Unknown.  
           Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
   AUTHORS Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.  
   TITLE Quantitative assay for the simultaneous detection and speciation of  
           bacterial infections  
   JOURNAL Patent: US 6699670-A 5 02-MAR-2004;  
           The Johns Hopkins University; Baltimore, MD  
 FEATURES Location/Qualifiers  
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           /organism="unknown"  
           /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 100.0%; Score 22; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
 |||||  
 Db 1 TGGAGCATGTGGTTTAATTCGA 22

## RESULT 4

AR154667  
 LOCUS AR154667 52 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 1 from patent US 6238927.  
 ACCESSION AR154667  
 VERSION AR154667.1 GI:15122720  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 52)  
 AUTHORS Abrams,E.S. and Hammond,P.W.  
 TITLE Reverse displacement assay for detection of nucleic acid sequences  
 JOURNAL Patent: US 6238927-A 1 29-MAY-2001;  
 FEATURES Location/Qualifiers  
 source 1..52  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCGA 22  
 |||||  
 Db 10 TGGAGCATGTGGTTTAATTCGA 31

## RESULT 5

AR159998/c  
 LOCUS AR159998 22 bp DNA linear PAT 17-OCT-2001  
 DEFINITION Sequence 2 from patent US 6251660.  
 ACCESSION AR159998  
 VERSION AR159998.1 GI:16222896  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Muir,A.R., Boles,T.Christian. and Adams,C.P.  
 TITLE Devices and methods for detecting target molecules in biological samples  
 JOURNAL Patent: US 6251660-A 2 26-JUN-2001;  
 FEATURES Location/Qualifiers  
 source 1..22  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGCATGTGGTTTAATTCG 21  
 |||||  
 Db 21 TGGAGCATGTGGTTTAATTCG 1

## RESULT 6

AR478761  
 LOCUS AR478761 22 bp DNA linear PAT 14-MAY-2004  
 DEFINITION Sequence 9 from patent US 6699670.  
 ACCESSION AR478761  
 VERSION AR478761.1 GI:47237481  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.  
 TITLE Quantitative assay for the simultaneous detection and speciation of bacterial infections  
 JOURNAL Patent: US 6699670-A 9 02-MAR-2004;  
 The Johns Hopkins University; Baltimore, MD  
 FEATURES Location/Qualifiers  
 source 1. .22  
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 /mol\_type="genomic DNA"

## ORIGIN

Query Match 92.7%; Score 20.4; DB 2; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 8e+05;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCGA 22  
 |||||  
 Db 1 TGGAGCATGCGGTTTAATTCGA 22

## RESULT 7

CQ818168  
 LOCUS CQ818168 22 bp DNA linear PAT 07-JUN-2004  
 DEFINITION Sequence 5 from Patent WO2004044247.  
 ACCESSION CQ818168  
 VERSION CQ818168.1 GI:48426960  
 KEYWORDS .  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Chaubron,F., Martin-Minvielle,A.C. and Groulon,S.  
 TITLE One step real-time rt pcr kits for the universal detection of organisms in industrial products  
 JOURNAL Patent: WO 2004044247-A 5 27-MAY-2004;  
 Genolife (FR)

FEATURES Location/Qualifiers  
 source 1. .22  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="#Description of artificial sequence:  
 oligonucleotide primer#"

## ORIGIN

Query Match 91.8%; Score 20.2; DB 2; Length 22;  
 Best Local Similarity 90.5%; Pred. No. 8.7e+05;  
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCG 21  
 :|||  
 Db 2 YGGAGCATGTGGYTTAATTCG 22

## RESULT 8

AX622955/c  
 LOCUS AX622955 24 bp DNA linear PAT 20-FEB-2003  
 DEFINITION Sequence 17 from Patent WO02095413.  
 ACCESSION AX622955  
 VERSION AX622955.1 GI:28450896  
 KEYWORDS .  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Brunham,R.C., Karunakaran,P. and Blanchard,J.  
 TITLE Diagnosis of vascular disease susceptibility using bacteriophage phi-cpn1 host chlamydia  
 JOURNAL Patent: WO 02095413-A 17 28-NOV-2002;  
 UNIVERSITY OF BRITISH COLUMBIA (CA)

FEATURES Location/Qualifiers  
 source 1. .24  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

/note="oligonucleotide primer for the 16s gene: reverse"

# ORIGIN

Query Match 90.9%; Score 20; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTC 20  
|||||  
Db 20 TGGAGCATGTGGTTTAATTC 1

## RESULT 9

AR089512  
LOCUS AR089512 25 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 271 from patent US 5994066.  
ACCESSION AR089512  
VERSION AR089512.1 GI:10016269  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.  
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories  
JOURNAL Patent: US 5994066-A 271 30-NOV-1999;  
FEATURES Location/Qualifiers  
source 1. .25  
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/mol\_type="unassigned DNA"

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Query Match 90.9%; Score 20; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTC 20  
|||||  
Db 6 TGGAGCATGTGGTTTAATTC 25

## RESULT 10

CS246054/c  
LOCUS CS246054 30 bp DNA linear PAT 09-JAN-2006  
DEFINITION Sequence 101 from Patent EP1609874.  
ACCESSION CS246054  
VERSION CS246054.1 GI:84660518  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Perseu,S.  
TITLE System for searching for and identifying pathogenic agents  
JOURNAL Patent: EP 1609874-A 101 28-DEC-2005;  
Bioanalisi Centro Sud S.n.c. di Perseu Sinibaldo eC. (IT)  
FEATURES Location/Qualifiers  
source 1. .30  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="probe"

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Best Local Similarity 100.0%; Pred. No. 9e+05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTC 20  
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Db 20 TGGAGCATGTGGTTTAATTC 1

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 15:45:05 ; Search time 212.707 Seconds  
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Title: US-10-743-384-2  
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 Sequence: 1 tgcgggacttaaccaaca 19

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Searched: 5244920 seqs, 3486124231 residues

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 Maximum Match 100%  
 Listing first 60 summaries

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 2: geneseqn1990s:  
 3: geneseqn2000s:  
 4: geneseqn2001as:  
 5: geneseqn2001bs:  
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 7: geneseqn2002bs:  
 8: geneseqn2003as:  
 9: geneseqn2003bs:  
 10: geneseqn2003cs:  
 11: geneseqn2003ds:  
 12: geneseqn2004as:  
 13: geneseqn2004bs:  
 14: geneseqn2005s:  
 15: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6 ABS71585	Abs71585 Reverse p
c 2	19	100.0	19	6 ABS71591	Abs71591 Bacterial

	3	19	100.0	19	12	ADO15326	Ado15326 PCR prime
	4	19	100.0	20	8	ACC48547	Acc48547 Affinity-
	5	19	100.0	21	2	AAT45274	Aat45274 Bacterial
	6	19	100.0	21	5	AAS11044	Aas11044 Bacterial
c	7	19	100.0	23	1	AAN82163	Aan82163 Sequence
c	8	19	100.0	23	2	AAV45647	Aav45647 Probe for
c	9	19	100.0	23	2	AAV62776	Aav62776 Probe for
c	10	19	100.0	23	3	AZ44009	Aaz44009 Enterobac
c	11	19	100.0	23	4	AAH44156	Aah44156 Escherich
	12	19	100.0	25	6	ABK90486	Abk90486 Synthetic
c	13	19	100.0	25	12	ADP47355	Adp47355 Intellige
c	14	19	100.0	25	12	ADQ59713	Adq59713 Intellige
c	15	19	100.0	25	14	AED28542	Aed28542 Primer fo
	16	19	100.0	26	1	AAN80834	Aan80834 Probe no.
	17	19	100.0	26	1	AAN97224	Aan97224 Probe con
	18	19	100.0	26	2	AAQ55675	Aaq55675 Amine lin
	19	19	100.0	26	2	AAT73684	Aat73684 RNA acrid
	20	19	100.0	26	2	AAT73680	Aat73680 Acridiniu
	21	19	100.0	26	2	AAT43265	Aat43265 Probe #4
	22	19	100.0	26	2	AAV01611	Aav01611 Linker-mo
c	23	19	100.0	26	2	AAV06803	Aav06803 Target ol
	24	19	100.0	26	2	AAV06802	Aav06802 Modified
	25	19	100.0	26	2	AAT86639	Aat86639 Oligonucl
	26	19	100.0	26	2	AZ09277	Aaz09277 Acridiniu
	27	19	100.0	26	3	AZ60216	Aaz60216 Probe #1
	28	19	100.0	26	3	AZ95615	Aaz95615 Linker re
	29	19	100.0	26	3	AZ95618	Aaz95618 Linker re
	30	19	100.0	26	4	AAH44126	Aah44126 DNA label
	31	19	100.0	26	4	AAH44125	Aah44125 DNA label
	32	19	100.0	26	4	AAH44128	Aah44128 RNA-alpha
	33	19	100.0	26	4	AAH44129	Aah44129 RNA-alpha
	34	19	100.0	26	4	AAH44127	Aah44127 DNA label
	35	19	100.0	26	4	AAH44130	Aah44130 RNA fragm
	36	19	100.0	26	5	AAF23080	Aaf23080 Campyloba
	37	19	100.0	26	5	AAF23102	Aaf23102 Bacterial
	38	19	100.0	26	6	ABK90484	Abk90484 Synthetic
c	39	19	100.0	26	6	ABK90485	Abk90485 Synthetic
	40	19	100.0	26	6	ABS52480	Abs52480 RNA seque
	41	19	100.0	26	6	ABS52479	Abs52479 DNA seque
	42	19	100.0	26	6	ABS52481	Abs52481 RNA seque
	43	19	100.0	26	6	ABS52482	Abs52482 RNA seque
	44	19	100.0	26	6	ABS52477	Abs52477 DNA seque
	45	19	100.0	26	6	ABS52478	Abs52478 DNA seque
c	46	19	100.0	26	8	ACC48545	Acc48545 Target RN
	47	19	100.0	26	8	ACC48546	Acc48546 Affinity-
c	48	19	100.0	51	12	ADO85475	Ado85475 Bacterial
c	49	19	100.0	59	2	AAV79269	Aav79269 Staphyloc
c	50	18	94.7	19	12	ADP47513	Adp47513 Intellige
c	51	18	94.7	19	12	ADP47583	Adp47583 Intellige
c	52	18	94.7	19	12	ADP47579	Adp47579 Intellige
c	53	18	94.7	19	12	ADP47585	Adp47585 Intellige
c	54	18	94.7	19	12	ADQ59871	Adq59871 Intellige
c	55	18	94.7	19	12	ADQ59943	Adq59943 Intellige
c	56	18	94.7	19	12	ADQ59941	Adq59941 Intellige
c	57	18	94.7	19	12	ADQ59937	Adq59937 Intellige
c	58	18	94.7	19	14	AED28541	Aed28541 Primer fo
c	59	18	94.7	55	8	ACC97177	Acc97177 Consensus
	60	17.4	91.6	26	5	AAF23118	Aaf23118 N. gonorr

## ALIGNMENTS

## RESULT 1

ABS71585

ID ABS71585 standard; DNA; 19 BP.

XX

AC ABS71585;

XX

DT 28-NOV-2002 (first entry)

XX

DE Reverse primer for detecting bacterial infection P1033R.

XX

KW Eubacteria; species detection; speciation; 16s RNA; PCR; primer; ss.

XX

OS Synthetic.

XX  
 PN WO200270728-A2.  
 .XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US006050.  
 XX  
 PR 01-MAR-2001; 2001US-0272642P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Rothman RE, Yang S, Lin S, Kelen GD;  
 XX  
 DR WPI; 2002-698755/75.  
 XX  
 PT Detecting and determining species source of eubacterial DNA in a sample,  
 PT comprises amplifying template DNA in the sample using a real-time  
 PT polymerase chain reaction with the use of primers and at least two  
 PT fluorogenic probes.  
 XX  
 PS Claim 12; Page 11; 39pp; English.  
 XX  
 CC The invention describes a method of detecting and determining species  
 CC source of eubacterial DNA in a sample. The method comprises amplifying  
 CC template DNA in the sample using a real-time polymerase chain reaction (R  
 CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at  
 CC least two fluorogenic probes. The methods are useful in detecting and  
 CC determining species source of eubacterial DNA in a sample. The present  
 CC method allows for highly sensitive detection of any eubacterial species  
 CC with simultaneous speciation. It eliminates false positive results in  
 CC detecting bacterial infections. This sequence represents a primer  
 CC designed using 16s RNA sequences and used in the eubacterial detection  
 CC method of the invention  
 XX  
 SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
  
 Query Match 100.0%; Score 19; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TGCGGGACTTAACCCAACA 19  
 ||||||||||||||||||  
 Db 1 TGCGGGACTTAACCCAACA 19

## RESULT 2

ABS71591/c

ID ABS71591 standard; DNA; 19 BP.

XX

AC ABS71591;

XX

DT 28-NOV-2002 (first entry)

XX

DE Bacterial 16s RNA fragment for primer design #4.

XX

KW Eubacteria; species detection; speciation; 16s RNA; ds.

XX

OS Staphylococcus aureus.

XX

PN WO200270728-A2.

XX

PD 12-SEP-2002.

XX

PF 01-MAR-2002; 2002WO-US006050.

XX

PR 01-MAR-2001; 2001US-0272642P.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Rothman RE, Yang S, Lin S, Kelen GD;

XX

DR WPI; 2002-698755/75.

XX

PT Detecting and determining species source of eubacterial DNA in a sample,

PT comprises amplifying template DNA in the sample using a real-time

PT polymerase chain reaction with the use of primers and at least two

PT fluorogenic probes.  
 XX  
 .PS Disclosure; Fig 5; 39pp; English.  
 XX  
 CC The invention describes a method of detecting and determining species  
 CC source of eubacterial DNA in a sample. The method comprises amplifying  
 CC template DNA in the sample using a real-time polymerase chain reaction (R  
 CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at  
 CC least two fluorogenic probes. The methods are useful in detecting and  
 CC determining species source of eubacterial DNA in a sample. The present  
 CC method allows for highly sensitive detection of any eubacterial species  
 CC with simultaneous speciation. It eliminates false positive results in  
 CC detecting bacterial infections. This sequence represents a bacterial 16s  
 CC RNA sequence used to create primers for use in the eubacterial detection  
 CC method of the invention  
 XX  
 SQ Sequence 19 BP; 3 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 19 TGCGGGACTTAACCCAACA 1

## RESULT 3

ADO15326

ID ADO15326 standard; DNA; 19 BP.

XX

AC ADO15326;

XX

DT 12-AUG-2004 (first entry)

XX

DE PCR primer used for one-step real-time RT-PCR detection SeqID 2.

XX

KW one step real-time RT-PCR; pharmaceutical; cosmetic; bacteria;

KW fungus-yeast; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO2004044247-A2.

XX

PD 27-MAY-2004.

XX

PF 03-NOV-2003; 2003WO-IB005312.

XX

PR 12-NOV-2002; 2002US-0425327P.

XX

PA (GENO-) GENOLIFE.

XX

PI Chaubron F, Martin-Minvielle AC, Groulon S;

XX

DR WPI; 2004-411742/38.

XX

PT Determining presence of bacteria or fungus-yeast RNA in sample involves

PT carrying out reverse transcriptase-PCR reaction of fungus-yeast RNA and

PT treating amplified DNA with probes which hybridize to amplified DNA.

XX

PS Claim 1; SEQ ID NO 2; 31pp; English.

XX

CC This invention relates to a novel method for one step real-time RT-PCR

CC kits useful for the detection of microorganisms occurring within

CC industrial products such as pharmaceuticals, cosmetic and non-clinical

CC samples. Specifically, it refers to determining the presence of bacteria

CC or fungus-yeast RNA in a sample suspected of containing such

CC contaminants. The present invention describes oligonucleotide primers and

CC probes that are natural nucleic acid or peptide nucleic acid (PNA)

CC molecules that can hybridise to the target nucleic acid (DNA and RNA).

CC Accordingly, the method enables rapid and simultaneous detection and

CC quantification of RNA from bacteria and fungus-yeast in either sterile or

CC non-sterile products in less than 24 hours. Furthermore, the one step

CC process reduces the risk of environmental contamination that could occur

CC when the reaction tubes are opened during the PCR procedure. This

CC oligonucleotide sequence is a PCR primer used in one-step real time RT-

CC PCR to amplify bacteria and fungus-yeast RNA, given in an exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 1 TGCGGGACTTAACCCAACA 19

#### RESULT 4 ACC48547

ID ACC48547 standard; DNA; 20 BP.  
 XX  
 AC ACC48547;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Affinity-labeled probe for nucleic acid detection.  
 XX  
 KW Nucleic acid detection; affinity-shifted probe; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 10. .11  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= labelled with acridinium ester"  
 XX  
 PN WO2003020952-A2.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027710.  
 XX  
 PR 31-AUG-2001; 2001US-0316770P.  
 PR 26-MAR-2002; 2002US-0368072P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Becker MM, Nelson NC;  
 XX  
 DR WPI; 2003-313092/30.  
 XX  
 PT Novel probe reagent for quantifying amount of analyte polynucleotide  
 PT present in test sample in lower or higher amounts, has two or more probes  
 PT that hybridize with same analyte polynucleotide with different  
 PT affinities.  
 XX  
 PS Example 1; Page 44; 84pp; English.  
 XX  
 CC The present invention relates to the use of multiple probes for  
 CC quantifying analytes over an extended dynamic range. To demonstrate the  
 CC basis of the quantitative approach underlying the invention, an  
 CC experiment was conducted using 3 types of hybridisation reaction, each  
 CC reaction being characterised by its own dynamic range. The present  
 CC sequence is that of a second probe used in the procedure. It is a 20-mer  
 CC labelled with acridinium ester (AE) to a specific activity of  $9.37 \times 10$   
 CC power 7 rlu/pmole. A first 26-mer probe (see ACC48547) was labelled with  
 CC AE to a specific activity of  $1.31 \times 10$  power 8 rlu/pmole. The target was  
 CC an RNA sequence (see ACC48545) from Escherichia coli. The first set of  
 CC hybridisation reactions included 0.5 fmol of the 26-mer probe, the second  
 CC set used 0.5 fmol of the 20-mer, and the third used 0.5 fmol of each  
 CC probe. The 26-mer and 20-mer probes were separately useful for  
 CC quantifying the analyte over 10-1,000 and 1,000-100,000 fmol ranges,  
 CC respectively, but together provided a quantitative range from 10 to  
 CC 100,000 fmol. The results showed how 2 different probes harbouring  
 CC indistinguishable labels and binding the same analyte with a different  
 CC measurable interaction can be used to quantify the analyte over an  
 CC extended dynamic range  
 XX

SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19

|||||

Db 1 TGC GGGACTTAACCCAACA 19

#### RESULT 5

AAT45274

ID AAT45274 standard; DNA; 21 BP.

XX

AC AAT45274;

XX

DT 06-AUG-1997 (first entry)

XX

DE Bacterial 16S rRNA V6 variable region amplification primer.

XX

KW Ribosomal RNA; 16S rRNA; V6 variable region; diagnostic probe;

KW species-specific; amplification primer; polymerase chain reaction; PCR;

KW Clavibacter michiganensis; ss.

XX

OS Synthetic.

XX

PN FR2733754-A1.

XX

PD 08-NOV-1996.

XX

PF 05-MAY-1995; 95FR-00005416.

XX

PR 05-MAY-1995; 95FR-00005416.

XX

PA (UYAN-) UNIV ANGERS.

XX

PI Horvais A;

XX

DR WPI; 1997-001737/01.

XX

PT Clavibacter michiganensis DNA fragments - useful as diagnostic probes and primers.

XX

PS Disclosure; Page 20; 29pp; French.

XX

CC Genomic DNA coding for the V6 variable region of 16S ribosomal RNA was amplified from 7 different bacterial strains using PCR primers having the sequences given in AAT45273 and AAT45274. The bacteria were divided into three groups: the first group contained 2 different sub-species of Clavibacter michiganensis; the second group contained 2 non-michiganensis Clavibacter species and the third group consisted of 3 varieties of Curtobacterium flaccumfaciens. The amplification products were sequenced and a consensus sequence was derived for each of the three groups. A comparison of the three consensus sequences allowed a sequence specific to C.michiganensis V6 variable region to be identified, i.e. the sequence in AAT45270. Single-stranded fragments which have at least 70% homology with the identified sequence or their complementary sequences are claimed. The new DNA fragments are used as probes and primers for detecting C.michiganensis infections, e.g. in tomatoes

XX

SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19

|||||

Db 2 TGC GGGACTTAACCCAACA 20

#### RESULT 6

AAS11044

ID AAS11044 standard; DNA; 21 BP.

XX

AC AAS11044;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Bacterial 16s RNA antisense oligomer #10.  
 XX  
 KW Antisense; bacterial 16s ribosomal RNA; rRNA; bacterial infection; human;  
 KW food grain supplement; livestock; poultry; therapeutic; ss.  
 XX  
 OS *Vibrio cholerae*.  
 OS *Escherichia coli*.  
 OS *Salmonella typhimurium*.  
 OS *Shigella dysenteriae*.  
 OS *Haemophilus influenzae*.  
 OS *Pseudomonas aeruginosa*.  
 OS *Neisseria gonorrhoeae*.  
 OS *Staphylococcus aureus*.  
 OS *Mycobacterium tuberculosis*.  
 OS *Helicobacter pylori*.  
 OS *Streptococcus pneumoniae*.  
 OS *Treponema pallidum*.  
 OS *Chlamydia trachomatis*.  
 OS *Bartonella henselae*.  
 XX  
 PN WO200142457-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 29-NOV-2000; 2000WO-US042391.  
 XX  
 PR 29-NOV-1999; 99US-0168150P.  
 XX  
 PA (AVIB-) AVI BIOPHARMA INC.  
 XX  
 PI Iversen PL;  
 XX  
 DR WPI; 2001-457295/49.  
 XX  
 PT Antibacterial compound, useful for treating bacterial infections and as  
 PT livestock and poultry food supplement, comprises antisense  
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA.  
 XX  
 PS Claim 11; Page 44; 62pp; English.  
 XX  
 CC AAS11035-AAS11157 represent the coding sequences of bacterial 16S  
 CC ribosomal RNA (rRNA) antisense oligomers. These sequences are  
 CC antibacterial compounds comprising substantially uncharged antisense  
 CC oligomers containing 8-40 nucleotide subunits, including a targeting  
 CC nucleic acid sequence at least 10 nucleotides in length which is  
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The  
 CC antisense oligomers are used for treating a bacterial infection in a  
 CC human or a mammalian animal produced by *Escherichia coli*, *Salmonella*  
 CC *typhimurium*, *Pseudomonas aeruginosa*, *Vibrio cholera*, *Neisseria*  
 CC *gonorrhoea*, *Helicobacter pylori*, *Bartonella henselae*, *Haemophilus*  
 CC *influenza*, *Shigella dysenteriae*, *Staphylococcus aureus*, *Mycobacterium*  
 CC *tuberculosis*, *Streptococcus pneumoniae*, *Treponema palladium* and *Chlamydia*  
 CC *trachomatis*. The antibacterial compound may be used as a food grain  
 CC supplement in livestock and poultry food composition. (Updated on 06-AUG-  
 CC 2003 to correct OS field.)  
 XX  
 SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
  
 Query Match 100.0%; Score 19; DB 5; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 2 TGCGGGACTTAACCCAACA 20

## RESULT 7

AAN82163/c

ID AAN82163 standard; DNA; 23 BP.

XX

AC AAN82163;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-DEC-1990 (first entry)  
 XX  
 DE Sequence #21 recognised by probe for 16S RNA gene of mycoplasma.  
 XX  
 KW Mollicutes.  
 XX  
 OS Mycoplasma.  
 XX  
 PN EP250662-A.  
 XX  
 PD 07-JAN-1988.  
 XX  
 PF 25-JUN-1986; 86EP-00304919.  
 XX  
 PR 25-JUN-1986; 86EP-00304919.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Gobel U, Stanbridge EJ;  
 XX  
 DR WPI; 1988-000726/01.  
 XX  
 PT Detection of prokaryotic organisms - esp. mycoplasma by hybridisation  
 PT with an oligo:nucleotide probe complementary to nucleotide sequence in  
 PT the prokaryote.  
 XX  
 PS Claim 16; Page 6; 9pp; English.  
 XX  
 CC A probe which is complementary to this sequence can be used to detect  
 CC prokaryotes. See also AAN82143-71. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX  
 SQ Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
 |||||  
 Db 19 TGC GGGACTTAACCCAACA 1

## RESULT 8

AAV45647/c

ID AAV45647 standard; DNA; 23 BP.

XX

AC AAV45647;

XX

DT 04-MAR-1999 (first entry)

XX

DE Probe for prokaryotic 16S RNA gene.

XX

 KW Probe; 16S RNA gene; mycoplasma; detection; prokaryote; diagnosis;  
 KW bacteriaemia; septicemia; ss.

XX

OS Synthetic.

XX

PN US5851767-A.

XX

PD 22-DEC-1998.

XX

PF 06-JUN-1995; 95US-00469600.

XX

PR 04-MAR-1985; 85US-00707725.

PR 06-MAY-1988; 88US-00191852.

PR 27-NOV-1991; 91US-00799856.

PR 19-FEB-1993; 93US-00020874.

PR 14-OCT-1993; 93US-00136723.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Stanbridge EJ, Gobel U;

XX  
 DR WPI; 1999-094418/08.  
 XX  
 PT Detection of mycoplasma-specific or prokaryote-specific nucleic acids -  
 PT using mycoplasma-specific or prokaryote-specific probes.  
 XX  
 PS Claim 3; Col 8; 11pp; English.  
 XX  
 CC This sequence represents a probe based on prokaryotic 16S RNA genes that  
 CC can be used in the method of the invention. The method is for detecting  
 CC the presence of prokaryotic specific nucleic acids, and comprises: (a)  
 CC contacting a medium, which may contain a nucleic acid or nucleic acid  
 CC fragment from the prokaryote having a particular nucleotide sequence,  
 CC with an oligonucleotide comprising a nucleotide sequence complementary to  
 CC the particular nucleotide sequence, whereby the oligonucleotide  
 CC hybridises with any nucleic acid or nucleic acid fragment from the  
 CC prokaryote which may be present in the medium; and (b) detecting the  
 CC presence of any nucleic acid or nucleic acid fragment hybridised with the  
 CC oligonucleotide. The invention also relates to a method for determining  
 CC the presence of a mycoplasma. The detection process is useful for  
 CC contaminated cell cultures or other biological environments. The probes  
 CC can be used in the diagnosis of bacteraemia or septicaemia in mammals.  
 CC The process provides a rapid, simple, effective, sensitive and specific  
 CC mycoplasma detection system. The probes can be made specific for  
 CC individual mycoplasma, acholeplasma, ureaplasma, spiroplasma, and  
 CC eubacterial species  
 XX  
 SQ Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGGGACTTAACCCAACA 19  
 ||||||||||||||||  
 Db 19 TCGGGGACTTAACCCAACA 1

## RESULT 9

AAV62776/c

ID AAV62776 standard; RNA; 23 BP.

XX

AC AAV62776;

XX

DT 04-MAR-1999 (first entry)

XX

DE Probe for prokaryotic 16S RNA gene.

XX

KW Probe; 16S RNA gene; mycoplasma; detection; prokaryote; diagnosis;  
 KW bacteraemia; septicaemia; ss.

XX

OS Synthetic.

XX

PN US5851767-A.

XX

PD 22-DEC-1998.

XX

PF 06-JUN-1995; 95US-00469600.

XX

PR 04-MAR-1985; 85US-00707725.

PR 06-MAY-1988; 88US-00191852.

PR 27-NOV-1991; 91US-00799856.

PR 19-FEB-1993; 93US-00020874.

PR 14-OCT-1993; 93US-00136723.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Stanbridge EJ, Gobel U;

XX

DR WPI; 1999-094418/08.

XX

PT Detection of mycoplasma-specific or prokaryote-specific nucleic acids -  
 PT using mycoplasma-specific or prokaryote-specific probes.

XX

PS Claim 19; Col 11; 11pp; English.

XX

CC This sequence represents a probe based on prokaryotic 16S RNA genes that  
 CC can be used in the method of the invention. The method is for detecting  
 CC the presence of prokaryotic specific nucleic acids, and comprises: (a)  
 CC contacting a medium, which may contain a nucleic acid or nucleic acid  
 CC fragment from the prokaryote having a particular nucleotide sequence,  
 CC with an oligonucleotide comprising a nucleotide sequence complementary to  
 CC the particular nucleotide sequence, whereby the oligonucleotide  
 CC hybridises with any nucleic acid or nucleic acid fragment from the  
 CC prokaryote which may be present in the medium; and (b) detecting the  
 CC presence of any nucleic acid or nucleic acid fragment hybridised with the  
 CC oligonucleotide. The invention also relates to a method for determining  
 CC the presence of a mycoplasma. The detection process is useful for  
 CC contaminated cell cultures or other biological environments. The probes  
 CC can be used in the diagnosis of bacteraemia or septicaemia in mammals.  
 CC The process provides a rapid, simple, effective, sensitive and specific  
 CC mycoplasma detection system. The probes can be made specific for  
 CC individual mycoplasma, acholeplasma, ureaplasma, spiroplasma, and  
 CC eubacterial species

XX

SQ Sequence 23 BP; 5 A; 5 C; 7 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19

|||||

Db 19 TGCGGGACTTAACCCAACA 1

## RESULT 10

AAZ44009/c

ID AAZ44009 standard; DNA; 23 BP.

XX

AC AAZ44009;

XX

DT 17-MAR-2000 (first entry)

XX

DE Enterobacteriaceae detecting probe #2.

XX

KW Detection; microorganism; primer; probe; cosmetic; food; ss.

XX

OS Bacteria.

XX

PN W09958713-A2.

XX

PD 18-NOV-1999.

XX

PF 10-MAY-1999; 99WO-DE001471.

XX

PR 12-MAY-1998; 98DE-01022108.

XX

PA (BIOI-) BIOINSIDE GMBH.

XX

PI Gerbling K, Lauter F, Grohmann L;

XX

DR WPI; 2000-072341/06.

XX

PT A test kit for detecting microbially soiled, non sterile products,  
 PT especially pharmaceuticals and cosmetics.

XX

PS Example 26; Page 77; 77pp; German.

XX

CC This invention describes a novel test kit to detect microbially soiled,  
 CC non-sterile products, in particular after GMP-rich lines, also in  
 CC cosmetics and food. The method involves the use of DNA fragment having a  
 CC forward primer, probe, a reverse primer and if necessary a spacer  
 CC oligonucleotide. The test kit and method are useful for economic  
 CC detection of germs in pharmaceutical and cosmetic products. In particular  
 CC the method is useful for detecting E. coli, P. aeruginosa, S. aureus and  
 CC Salmonella

XX

SQ Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 3; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
 |||||  
 Db 20 TGC GGGACTTAACCCAACA 2

## RESULT 11

AAH44156/c

ID AAH44156 standard; DNA; 23 BP.

XX

AC AAH44156;

XX

DT 14-SEP-2001 (first entry)

XX

DE Escherichia coli 16S RNA gene oligonucleotide #10.

XX

KW Mycoplasma; 16S RNA gene; infection; biological probe; detection;  
 KW ribosomal RNA gene; prokaryote; ss.

XX

OS Escherichia coli.

XX

PN US6245509-B1.

XX

PD 12-JUN-2001.

XX

PF 14-SEP-1998; 98US-00152375.

XX

PR 04-MAR-1985; 85US-00707725.

PR 06-MAY-1988; 88US-00191852.

PR 27-NOV-1991; 91US-00799856.

PR 19-FEB-1993; 93US-00020874.

PR 14-OCT-1993; 93US-00136723.

PR 06-JUN-1995; 95US-00469600.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Stanbridge EJ, Gobel UB;

XX

DR WPI; 2001-416908/44.

XX

PT Generating oligonucleotide probes, which are useful in DNA hybridization  
 PT techniques for detecting mycoplasmas or prokaryotes in general.

XX

PS Disclosure; Col 2; 6pp; English.

XX

CC The present invention describes a method for obtaining oligonucleotide  
 CC probes, comprising synthesising and isolating an oligonucleotide  
 CC comprising a sequence identical to a sequence identified as hybridisable  
 CC under predetermined conditions to a nucleotide sequence from one or more  
 CC target organisms. The oligonucleotide probes are hybridisable to a  
 CC nucleotide sequence contained by or specific to one or more target  
 CC organisms but not to one or more selected non-target organisms in a  
 CC sample. The target and non-target organisms do not have a cellular  
 CC nucleus or are no higher phylogenetically than prokaryotes. The method  
 CC comprises: (a) obtaining particular nucleotide sequence information of  
 CC one or more of the target organisms; (b) obtaining particular nucleotide  
 CC sequence information of one or more of the selected non-target organisms;  
 CC (c) comparing the target and non-target sequence information and  
 CC identifying from it at least one oligonucleotide sequence that is  
 CC hybridisable under the predetermined conditions to a nucleotide sequence  
 CC from the target organisms, but not to a nucleotide sequence of non-target  
 CC organisms; and (d) synthesising and isolating an oligonucleotide  
 CC comprising a sequence identical to the identified sequence. The method  
 CC can be used for generating oligonucleotide probes for detecting  
 CC mycoplasmas or prokaryotes in general. The present sequence represents an  
 CC Escherichia coli 16S RNA gene oligonucleotide which is given in the  
 CC exemplification of the present invention

XX

SQ Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19

Db                   |||||||  
19 TGCGGGACTTAACCCAACA 1

## RESULT 12

ABK90486

ID   ABK90486 standard; DNA; 25 BP.

XX

AC   ABK90486;

XX

DT   05-NOV-2002   (first entry)

XX

DE   Synthetic polynucleotide probe #2.

XX

KW   Polycationic polymer; nucleic acid hybridisation; probe; ss;

KW   disease-associated gene; polymorphism.

XX

OS   Synthetic.

XX

PN   WO200248404-A2.

XX

PD   20-JUN-2002.

XX

PF   07-DEC-2001; 2001WO-US048592.

XX

PR   14-DEC-2000; 2000US-0255535P.

XX

PA   (GENP-) GEN-PROBE INC.

XX

PI   Becker MM;

XX

DR   WPI; 2002-608283/65.

XX

PT   Forming duplexes from probe and target nucleic acid for diagnosing  
PT   presence or absence of virus or organism in a sample, by conducting  
PT   hybridization between the two in the presence of a synthetic polycationic  
PT   polymer.

XX

PS   Example 2; Page 49; 63pp; English.

XX

CC   The invention relates to forming a duplex from a polynucleotide probe and  
CC   a target nucleic acid comprising providing the probe to a test sample  
CC   under conditions permitting the probe to preferentially hybridise to the  
CC   target nucleic acid in the sample and providing a synthetic polycationic  
CC   polymer to the sample which increases the association rate of the probe  
CC   and the target nucleic acid. The method is useful for forming a duplex  
CC   from a probe and a target nucleic acid comprising RNA (mRNA or rRNA). The  
CC   probe preferentially hybridises to a target nucleic acid sequence  
CC   contained in the target nucleic acid under the conditions, which is  
CC   useful for diagnosing the presence or absence of a virus or organism or  
CC   members of a group of viruses or organisms in the sample. The method is  
CC   also useful for detecting the presence of a disease-associated gene,  
CC   determining the state of a disease, measuring levels of gene expression  
CC   and detecting mutations or polymorphisms in a test sample. This sequence  
CC   represents a probe used in the method of the invention

XX

SQ   Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match                   100.0%;   Score 19;   DB 6;   Length 25;

Best Local Similarity   100.0%;   Pred. No. 2.5;

Matches   19;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy                   1 TGCGGGACTTAACCCAACA 19

Db                   |||||||

6 TGCGGGACTTAACCCAACA 24

## RESULT 13

ADP47355/c

ID   ADP47355 standard; DNA; 25 BP.

XX

AC   ADP47355;

XX

DT   09-SEP-2004   (first entry)

XX

DE   Intelligent PCR primer for the identification of bacteria SeqID 10.

XX  
 KW PCR; ss; primer; pharmacogenetic analysis; medical diagnosis; cancer;  
 KW blood typing; virus stereotyping; pathogen; mass spectroscopy;  
 KW etiologic agent.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004052175-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 05-DEC-2003; 2003WO-US038830.  
 XX  
 PR 06-DEC-2002; 2002US-0431319P.  
 PR 18-DEC-2002; 2002US-00323233.  
 PR 18-DEC-2002; 2002US-00325526.  
 PR 18-DEC-2002; 2002US-00325527.  
 PR 18-DEC-2002; 2002US-00326051.  
 PR 29-JAN-2003; 2003US-0443443P.  
 PR 30-JAN-2003; 2003US-0443788P.  
 PR 14-FEB-2003; 2003US-0447529P.  
 PR 11-SEP-2003; 2003US-00660122.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Ecker DJ, Griffey RH, Hofstadler SA, Sampath R, Mcneil J;  
 PI Crooke ST;  
 XX  
 DR WPI; 2004-468672/44.  
 XX  
 PT Identifying a pathogen in a biological sample, useful in medical  
 PT diagnosis, comprises amplifying a nucleic acid from the sample with a  
 PT pair of intelligent primers, and determining the molecular mass of the  
 PT amplification product.  
 XX  
 PS Example 15; SEQ ID NO 10; 228pp; English.  
 XX  
 CC This invention relates to a novel method for the rapid identification of  
 CC pathogens occurring in environmental samples or biological samples  
 CC derived from humans and animals. Specifically, it refers to using  
 CC intelligent primers to obtain an amplification product in order that the  
 CC molecular mass of the amplicon can be determined by mass spectroscopy,  
 CC which in turn identifies the pathogen found in the sample. The present  
 CC invention describes the rapid detection and identification of an  
 CC etiologic agent that does not required nucleic acid sequencing, and  
 CC instead relies on the use of intelligent primers to target ribosomal RNA  
 CC or housekeeping genes. Accordingly, this method can be used to identify a  
 CC pathogen or infectious agent in a biological sample, which is useful in  
 CC pharmacogenetic analysis and medical diagnosis (including cancer  
 CC diagnosis based on mutations and polymorphisms), or for detecting single  
 CC nucleotide polymorphisms in blood typing or stereotyping of viruses. This  
 CC oligonucleotide sequence is an intelligent PCR primer used to identify  
 CC different bacterial strains, given in an exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGGGACTTAACCCAACA 19  
 |||||  
 Db 20 TCGGGGACTTAACCCAACA 2

## RESULT 14

ADQ59713/c

ID ADQ59713 standard; DNA; 25 BP.

XX

AC ADQ59713;

XX

DT 07-OCT-2004 (first entry)

XX

DE Intelligent PCR primer 16S\_EC\_1082\_1197 forward SEQ ID NO:10.

XX

KW ss; etiologic agent; disease; intelligent primer;  
 KW pathogen identification; PCR; primer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004060278-A2.  
 XX  
 PD 22-JUL-2004.  
 XX  
 PF 05-DEC-2003; 2003WO-US038761.  
 XX  
 PR 06-DEC-2002; 2002US-0431319P.  
 PR 18-DEC-2002; 2002US-00323233.  
 PR 18-DEC-2002; 2002US-00325526.  
 PR 18-DEC-2002; 2002US-00325527.  
 PR 18-DEC-2002; 2002US-00326051.  
 PR 29-JAN-2003; 2003US-0443443P.  
 PR 30-JAN-2003; 2003US-0443788P.  
 PR 14-FEB-2003; 2003US-0447529P.  
 PR 11-SEP-2003; 2003US-0501926P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Ecker DJ, Griffey RH, Sampath R, Hofstadler SA, Mcneil J;  
 PI Crooke ST, Blyn LB, Ranken R, Hall TA;  
 XX  
 DR WPI; 2004-534302/51.  
 XX  
 PT Identifying pathogens in humans or animals comprises amplifying a nucleic  
 PT acid molecule from the individual with intelligent primers to obtain  
 PT amplification products, and determining molecular masses of the  
 PT amplification products.  
 XX  
 PS Claim 40; SEQ ID NO 10; 184pp; English.  
 XX  
 CC The invention relates to a novel method for identifying etiologic agents  
 CC of disease in an individual comprising amplifying a nucleic acid from a  
 CC biological sample of the individual with intelligent primers to obtain  
 CC amplification products corresponding to the etiologic agents, and  
 CC determining the molecular masses of the amplification products. The  
 CC composition and methods of the invention are useful for identifying  
 CC pathogens in biological samples from humans and animals, resolving  
 CC etiologic agents present in samples obtained from humans and animals,  
 CC determining detailed genetic information about such pathogens or  
 CC etiologic agents, and for rapidly detecting and identifying bioagents  
 CC from environmental, clinical or other samples. The present sequence  
 CC represents an intelligent PCR primer of the invention.  
 XX  
 SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGC GGGACTTAACCCAACA 19  
 |||  
 Db 20 TGC GGGACTTAACCCAACA 2

## RESULT 15

AED28542/c

ID AED28542 standard; DNA; 25 BP.

XX

AC AED28542;

XX

DT 15-DEC-2005 (first entry)

XX

DE Primer for PCR detection of 16S ribosomal RNA, SEQ ID NO:3.

XX

KW Microorganism detection; biological warfare; DNA identification;

KW DNA amplification; ss; primer; PCR; 16S ribosomal RNA.

XX

OS Escherichia coli.

XX

PN WO2005098047-A2.

XX

PD 20-OCT-2005.  
 XX  
 PF 18-FEB-2005; 2005WO-US005356.  
 XX  
 PR 18-FEB-2004; 2004US-0545425P.  
 PR 05-APR-2004; 2004US-0559754P.  
 PR 03-DEC-2004; 2004US-0632862P.  
 PR 22-DEC-2004; 2004US-0639068P.  
 PR 28-JAN-2005; 2005US-0648188P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 PA (SCIT-) SCI APPL INT CORP.  
 XX  
 PI Sampath R, Hall TA, Ecker DJ, Eschoo MW, Massire C, Larson BM;  
 PI Leighton T;  
 XX  
 DR WPI; 2005-703571/72.  
 XX  
 PT New oligonucleotide primer having a non-template tag, useful in preparing  
 PT a composition for determining the presence or absence of a bacterium of a  
 PT particular class, genus, species, or sub-species in a sample.  
 XX  
 PS Example 1; SEQ ID NO 3; 260pp; English.  
 XX  
 CC The new invention relates to genetic identification of bacteria.  
 CC Specifically claimed is a new oligonucleotide primer which has at least  
 CC one non-template tag. The primers are designed to produce bacterial  
 CC bioagent identifying amplicons of DNA encoding genes essential to life,  
 CC such as 16S, 23S rRNA, DNA-directed RNA polymerase subunits (rpoB and  
 CC rpoC), valyl-tRNA synthetase (vals), elongation factor EF-Tu (TufB),  
 CC ribosomal protein L2 (rplB), protein chain initiation factor (infB), and  
 CC spore protein (sspE). Also given is a composition comprising 1, 2 or more  
 CC of the oligonucleotide primers; a kit comprising the composition; a  
 CC method for identifying an unknown bacterium; a method of determining the  
 CC presence or absence of a bacterium of a particular class, genus, species,  
 CC or sub-species in a sample; and a method for determining the quantity of  
 CC an unknown bacterium in a sample. Either or both of the oligonucleotide  
 CC primers comprises at least one modified nucleobase, a non-templated T  
 CC residue on the 5'-end, at least one non-template tag, molecular mass  
 CC modifying tag or modified nucleobase. The oligonucleotide primers are  
 CC useful in preparing a composition for identifying an unknown bacterium,  
 CC determining the presence or absence of a bacterium of a particular class,  
 CC genus, species, or sub-species in a sample or determining the quantity of  
 CC an unknown bacterium in a sample. The present sequence is a primer from a  
 CC collection of primers used to identify bacteria using the described  
 CC methods. This primer detects a region of the gene encoding 16S ribosomal  
 CC RNA in an E.coli reference sequence.  
 XX  
 SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 20 TGCGGGACTTAACCCAACA 2

## RESULT 16

AAN80834

ID AAN80834 standard; DNA; 26 BP.

XX

AC AAN80834;

XX

DT 25-MAR-2003 (revised)

DT 30-NOV-1990 (first entry)

XX

DE Probe no.3 for 16S rRNA of a broad phylogenetic range of bacteria.

XX

KW Bacteria; probe; 16S ribosomal RNA; ss.

XX

OS Synthetic.

XX

PN W08803957-A.

XX

PD 02-JUN-1988.  
 XX  
 PF 24-NOV-1987; 87WO-US003009.  
 XX  
 PR 24-NOV-1986; 86US-00934244.  
 PR 07-AUG-1987; 87US-00083542.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PA (HOGA/) HOGAN J J.  
 XX  
 DR WPI; 1988-161626/23.  
 XX  
 PT Probes for non-viral organisms - comprising an oligo:nucleotide  
 PT complementary to a unique variable region r RNA sequence.  
 XX  
 PS Claim 221; Page 161; 211pp; English.  
 XX  
 CC The probe is designed to hybridise with 16S rRNA from a broad range of  
 CC bacteria commonly found in urine but not to yeast or human rRNA. It  
 CC corresponds to bases 1080-1110 of the E. coli 16S RNA and has a Tm of 67  
 CC deg.C. See also AAN80785-N80851. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX  
 SQ Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19  
 |||||  
 Db 7 TGCGGGACTTAACCCAACA 25

## RESULT 17

AAN97224

ID AAN97224 standard; DNA; 26 BP.

XX

AC AAN97224;

XX

DT 06-JUL-1993 (first entry)

XX

DE Probe contg. 5'-amine linker-arm.

XX

KW Deoxyoligonucleotide; probe; amine; label; acridinium ester; AE;  
 KW hybridisation assay; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /note= "comprises NH2-(CH2)6 as 5'-amine linker-arm"

XX

PN W08902476-A.

XX

PD 23-MAR-1989.

XX

PF 21-SEP-1988; 88WO-US003195.

XX

PR 21-SEP-1987; 87US-00099392.

XX

PA (MLTE-) ML TECHN VENTURES.

XX

PI Arnold L, Nelson NC;

XX

DR WPI; 1989-100016/13.

XX

PT Homogeneous binding assay using degradable label esp. acridinium ester -  
 PT with different stabilities in bound and unbound forms, esp. useful in  
 PT hybridisation detection of specific polynucleotide.

XX

PS Example 1(i); Page 20; 64pp; English.

XX

CC Deoxyoligonucleotide probes were synthesised to contain an amine linker-  
 CC arm (i.e., one which terminates in a primary amine for labelling with

CC acridinium ester) located either at the 5'-terminus, at a specific  
 CC preselected location along the polyphosphate chain, in the internal  
 CC portion of the probe or attached to one of the nucleotide bases.  
 CC Chemiluminescent acridinium ester labelled probes are used in homogeneous  
 CC hybridisation assay format for sensitively detecting the presence of  
 CC complementary target polynucleotide sequences

XX

SQ Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19

|||||

Db 7 TGC GGGACTTAACCCAACA 25

# RESULT 18

AAQ55675

ID AAQ55675 standard; DNA; 26 BP.

XX

AC AAQ55675;

XX

DT 25-MAR-2003 (revised)

DT 09-AUG-1994 (first entry)

XX

DE Amine linker containing probe #1.

XX

KW Probe; amine; linker arm; N-acridinium; ester; label; homogeneous;

KW hybridisation assay; detection; linear dilution series; Chlamydia; rRNA;

KW ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /label= NH2-(CH2)6-G

FT /note= "Amine linker arm"

XX

PN US5283174-A.

XX

PD 01-FEB-1994.

XX

PF 08-NOV-1990; 90US-00613603.

XX

PR 21-SEP-1987; 87US-00099392.

PR 12-DEC-1988; 88US-00294700.

PR 23-MAY-1990; 90US-00528920.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Nelson NC, Arnold LJ;

XX

DR WPI; 1994-048084/06.

XX

PT Homogeneous nucleic acid hybridisation assay - using probe labelled with

PT acridinium ester for detection of linear dilution series.

XX

PS Example 1; Col 12; 20pp; English.

XX

CC This sequence represents a probe which contains an amine linker arm which

CC may bear an N-acridinium ester label. Probes such as this may be used in

CC an homogeneous hybridisation assay for determining the presence or amount

CC of a target nucleic acid in a sample. This method comprises contacting

CC the sample with a probe such as this, such that the acridinium ester

CC label may be degraded by a chemical, eg. acid, base or oxidising agent,

CC while duplex-linked N-acridinium ester remains undegraded. The

CC hybridisation mixture is treated with the chemical and the amount of

CC undegraded N-acridinium ester is measured without physically separating

CC any unhybridised probe. The method is capable of detecting linear

CC dilution series, eg. Chlamydia rRNA with a detection limit of 0.1-1 ng.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGC GGGACTTAACCCAACA 19  
 |||||  
 Db 7 TGC GGGACTTAACCCAACA 25

## RESULT 19

AAT73684

ID AAT73684 standard; RNA; 26 BP.

XX

AC AAT73684;

XX

DT 05-SEP-1997 (first entry)

XX

DE RNA acridinium ester-labelled probe for adduct protection assay.

XX

KW probe; assay; analyte; adduct protection; detection; acridinium ester;

KW nucleic acid hybridisation; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc\_feature complement(1..26)

FT /\*tag= b

FT /note= "used as target sequence - no label"

FT modified\_base 16

FT /\*tag= a

FT /note= "Acridinium ester labelled uracil"

XX

PN EP747706-A1.

XX

PD 11-DEC-1996.

XX

PF 03-JUN-1996; 96EP-00108880.

XX

PR 07-JUN-1995; 95US-00478221.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Becker M, Nelson NC;

XX

DR WPI; 1997-023324/03.

XX

PT Specific binding assay using signal-altering reagent - that

PT preferentially alters signal of unbound probe.

XX

PS Example 5; Page 16; 37pp; English.

XX

CC Assaying for the presence of an analyte in a sample comprises using an  
 CC adduct protection assay involving the use of a labelled binding partner  
 CC and a signal altering ligand. The signal altering ligand can alter the  
 CC signal from the label to a greater extent when the labelled binding  
 CC partner is unbound than when it is bound to the analyte. The presence or  
 CC amount of analyte can be determined by detecting the signal produced from  
 CC unaltered label. The process is used especially for detecting nucleic  
 CC acid (esp. RNA) sequences by homogeneous hybridisation assay. The assay  
 CC is versatile, e.g. signal alteration can be effected under a wide range  
 CC of conditions (e.g. pH, temperature and ionic strength) and both signal  
 CC alteration and signal triggering can be effected at constant temperature  
 CC to achieve high sensitivity. The relationship between adduct formation  
 CC rates and the type of nucleic acid (RNA or DNA) present in the probe or  
 CC target has been examined. It was found that adduct formation rates depend  
 CC upon whether a probe and/or target is DNA or RNA and these rates do not  
 CC directly correlate with the corresponding hydrolysis rates of labels  
 CC identically associated with these molecules. The present sequence is an  
 CC RNA AE-labelled probe

XX

SQ Sequence 26 BP; 6 A; 8 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 26;  
 Best Local Similarity 84.2%; Pred. No. 2.5;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 TGCGGGACTTAACCCAACA 19
        :|||||||:|||||||
Db      7 UGCGGGACUUAACCCAACA 25

```

## RESULT 20

AAT73680

ID AAT73680 standard; DNA; 26 BP.

XX

AC AAT73680;

XX

DT 05-SEP-1997 (first entry)

XX

DE Acridinium ester labelled probe 3 for adduct protection assay.

XX

KW probe; assay; analyte; adduct protection; detection; acridinium ester;  
 KW nucleic acid hybridisation; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc\_feature complement(1..26)

FT /\*tag= b

FT /note= "used as target sequence - no label"

FT modified\_base 16

FT /\*tag= a

FT /note= "Acridinium ester labelled thymine"

XX

PN EP747706-A1.

XX

PD 11-DEC-1996.

XX

PF 03-JUN-1996; 96EP-00108880.

XX

PR 07-JUN-1995; 95US-00478221.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Becker M, Nelson NC;

XX

DR WPI; 1997-023324/03.

XX

PT Specific binding assay using signal-altering reagent - that  
 PT preferentially alters signal of unbound probe.

XX

PS Example 3; Page 13; 37pp; English.

XX

CC Assaying for the presence of an analyte in a sample comprises using an  
 CC adduct protection assay involving the use of a labelled binding partner  
 CC and a signal altering ligand. The signal altering ligand can alter the  
 CC signal from the label to a greater extent when the labelled binding  
 CC partner is unbound than when it is bound to the analyte. The presence or  
 CC amount of analyte can be determined by detecting the signal produced from  
 CC unaltered label. The process is used especially for detecting nucleic  
 CC acid (esp. RNA) sequences by homogeneous hybridisation assay. The assay  
 CC is versatile, e.g. signal alteration can be effected under a wide range  
 CC of conditions (e.g. pH, temperature and ionic strength) and both signal  
 CC alteration and signal triggering can be effected at constant temperature  
 CC to achieve high sensitivity. The effect different acridinium ester (AE)  
 CC derivative structures have on adduct formation rates was measured using  
 CC the present sequence as the AE-labelled probe and its complement as the  
 CC target. AE having unsubstituted acridinium rings form adducts with sodium  
 CC sulphite and metabisulphite at about the same rate. In contrast 1-methyl-  
 CC AE and 2,7-di-methyl-AE formed adducts more than ten times slower than  
 CC the unsubstituted AE derivatives

XX

SQ Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 TGCGGGACTTAACCCAACA 19
        |||||
Db      7 TGCGGGACTTAACCCAACA 25

```

Search completed: July 26, 2006, 15:58:55  
Job time : 214.707 secs

SCORE 1.3 BuildDate: 12/06/2005
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BN): X87272  
 GenBank VERSION (VER): X87272.1 GI:1165003  
 CAS REGISTRY NO. (RN): 172819-38-4  
 SEQUENCE LENGTH (SQL): 1484  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 22 Jan 1996  
 DEFINITION (DEF): B.japonicum 16S rRNA gene.  
 SOURCE: Bradyrhizobium japonicum.  
 ORGANISM (ORGN): Bradyrhizobium japonicum  
 Bacteria; Proteobacteria; alpha subdivision;  
 Rhizobiaceae group; Bradyrhizobium group;  
 Bradyrhizobium  
 NUCLEIC ACID COUNT (NA): 361 a 356 c 465 g 298 t 4 others  
 REFERENCE: 1 (bases 1 to 1484)  
 AUTHOR (AU): Ludwig,W.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (18-MAY-1995) W. Ludwig, Lehrstuhl fuer  
 Mikrobiologie, Technische Universitaet Muenchen,  
 Muenchen, FRG  
 REFERENCE: 2 (bases 1 to 1484)  
 AUTHOR (AU): Ludwig,W.; Rossello-Mora,R.; Aznar,R.; Klugbauer,S.;  
 Spring,S.; Reetz,K.; Beimfohr,C.; Brockmann,E.;  
 Kirchhof,G.; Dorn,S.; Bachleitner,M.; Klugbauer,N.;  
 Springer,N.; Lane,D.; Nietupsky,R.; Weizenegger,M.;  
 Schleifer,K.H.  
 TITLE (TI): Comparative sequence analysis of 23S rRNA from  
 proteobacteria  
 JOURNAL (SO): Syst. Appl. Microbiol., 18, 164-188 (1995)  
 OTHER SOURCE (OS): CA 124:195266

# FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1484	/organism="Bradyrhizobium japonicum" /strain="DSM 30131 T" /db-xref="taxon:375"
rRNA	1..1484	/gene="16S rRNA" /product="16S ribosomal RNA"
gene	1..1484	/gene="16S rRNA"

# SEQUENCE (SEQ):

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121 tcggaacaac acagggaaac ttgtgctaata accggataag cccttacggg gaaagattta
181 tcgccgaaaag atcgggccgc gtctgattag ctagtggta gggtaacggc ctaccaaggc
241 gacgatcagt agctggctctg agaggatgat cagccacatt gggactgaga cacggcccaa
301 actcctacgg gaggcagcag tggggaatat tggacaatgg gggcaaccct gatccagcca
361 tgccgcgtga gtgatgaagg ccctagggtt gtaaagctct tttgtgcggg aagataatga
421 cggtaccgca agaataagcc ccggctaact tcgtgccagc agccgcggta atacgaaggg
481 ggctagcggt gctcggaatc actgggcgta aagggtgcgt aggcgggtct ttaagtcagg
541 ggtgaaatcc tggagctcaa ctccagaact gcctttgata ctgaagatct tgagttcggg
601 agagggtgagt ggaactgcga gtgtagaggt gaaattcgta gatattcgca agaacaccag
661 tggcgaaggc ggctcactgg ccgcatactg acgctgaggc acgaaagcgt ggggagcaaa
721 caggattaga taccctggta gtccacgccg taaacgatga atgccagccg ttagtggggt
781 tactcactag tggcgagct aacgctttaa gcattccgcc tggggagtag ggtcgcaaga
841 ttaaaactca aaggaattga cgggggcccc cacaagcggg ggagcatgtg gtttaattcg
901 acgcaacgcg cagaacctta ccagcccttg acatgtccag gaccggctgc agagatgtga
961 ccttctcttc ggagcctgga acacagggtg tgcattggct tcgtcagctc gtgtcgtgag
1021 atgttggggt aagtcgca acgagcgcaa ccccgctc tagttgctac catttagttg
1081 agcactctaa ggagactgcc ggtgataagc cgcgaggaag gtggggatga cgtcaagtcc
1141 tcatggccct tacgggctgg gctacacacg tgctacaatg gcggtgacaa tgggatgcta
  
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Bradyrhizobium japonicum gene for 16S rRNA, strain: IAM  
12608.

SOURCE: Bradyrhizobium japonicum  
ORGANISM (ORGN): Bradyrhizobium japonicum

Bacteria; Proteobacteria; Alphaproteobacteria;  
Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium

REFERENCE: 1 (bases 1 to 1441)

AUTHOR (AU): Yanagi,M.; Yamasato,K.

TITLE (TI): Phylogenetic analysis of the family Rhizobiaceae and  
related bacteria by sequencing of 16S rRNA gene using  
PCR and DNA sequencer

JOURNAL (SO): FEMS Microbiol. Lett., 107 (1), 115-120 (1993)

OTHER SOURCE (OS): CA 119:155937

REFERENCE: 2 (bases 1 to 1441)

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1201 aggggcgacc cttcgcaaat ctcaaaaagc cgtctcagtt cggattgggc tctgcaactc
1261 gagcccatga agttggaatc gctagtaatc gtggatcagc acgccacggt gaatacgttc
1321 ccgggccttg tacacaccgc ccgtcacacc atgggagttg gctttacctg aagacggtgc
1381 gctaacctgc aaaggaggca gccggccacg gtagggtcag cgactggggt gaagtcgtaa
1441 caaggtagcc gtaggggaac ctgcggctgg atcacctcct ttnn

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L2 ANSWER 2 OF 2 GENBANK® COPYRIGHT 2006 on STN

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LOCUS (LOC):          BJ23SRRN      GenBank (R)
GenBank ACC. NO. (GBN): X71840
GenBank VERSION (VER): X71840.1  GI:468567
CAS REGISTRY NO. (RN): 154450-08-5
SEQUENCE LENGTH (SQL): 2882
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Bacteria
DATE (DATE):          28 Mar 1994
DEFINITION (DEF):     B.japonicum 16S rRNA gene.
SOURCE:               Bradyrhizobium japonicum.
  ORGANISM (ORGN):    Bradyrhizobium japonicum
                      Bacteria; Proteobacteria; alpha subdivision;
                      Rhizobiaceae group; Bradyrhizobium group;
                      Bradyrhizobium
NUCLEIC ACID COUNT (NA): 751 a   656 c   887 g   588 t
REFERENCE:            1 (bases 1 to 2882)
  AUTHOR (AU):        Springer,N.; Ludwig,W.; Hardarson,G.
  TITLE (TI):          A 23S rRNA targeted specific hybridization probe for
                      Bradyrhizobium japonicum
  JOURNAL (SO):        Syst. Appl. Microbiol., 16, 468-470 (1993)
  OTHER SOURCE (OS):   CA 120:262524
REFERENCE:            2 (bases 1 to 2882)
  AUTHOR (AU):        Ludwig,W.
  TITLE (TI):          Direct Submission
  JOURNAL (SO):        Submitted (05-MAY-1993) W. Ludwig, Lehrst. f.
                      Mikrobiologie TU Muenchen, Arcisstr. 21, 8000 Muenchen
                      2, FRG

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# FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2882	/organism="Bradyrhizobium japonicum" /strain="DSM 30131" /db-xref="taxon:375"
rRNA	1..2882	/product="23S ribosomal RNA"

# SEQUENCE (SEQ):

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1 aatcaagtgc cttaaggggtg ttcggtggat gccttggcgc tgagaggcga tgaaggacgt
61 gctacgctgc gataagccgt ggggagctgc gaagaagctt tgatccatgg atttccgaat
121 ggggaaaccc accttcgata gccggaactc caagaccttt gtcgaaagac atcgggtgtg
181 ggttcgatca gatgatgtga gaagccaggc ctttagattt cgatcgaaga ggttttggat
241 ttccggttat caagagaagg tatgagactt ctgaatacat aggaggtttc aagcaaaccc
301 aggggaactga aacatctaag tacctggagg aaaggacatc aacagagact ccgttagtag
361 tggcgaagcga acgcggacca ggccagtgat acatcaaaga caatcggaac cggtcaggaa
421 agccgggcct cagaggggtga tagccccgta cgagtaatgc gatgatgtat ccacgagtaa
481 ggcgggacac gtgaaatcct gtctgaacgc ggggggacca ccctccaagc ctaagtactc
541 ctgagcgacc gatagtgaac cagtaccgtg agggaaaggt gaaaagcacc ccgacgaggg
601 gagtgaataa gacctgaaac cggacaccta caaacagatg gagcccaaga tacgttctgg
661 gtgacatcgt accttttgta ttatgggcca gcgacttaat ttaacgagca agcttaagcc
721 gataggtgta ggcgcacgga aagcgagtct gaatagggcg tcaagttcgt tgtattagac
781 ccgaaacctg gtgatctagc catgagcagg ttgaaggtga ggtaacactc actggaggac
841 cgaacgggtg cctgttgaaa aaggctccga tgacttgtgg ttaggggtga aaggccaatc
901 aaactgggaa atagctgggt ctccgcgaaa gatatttagg tagcgctcgc gatgaatacc
961 tcagggggta gagcactgga tgggctaggg ggacttaccg tcttaccaaa cccaacaaa

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1021	ctccgaatac	ctgagagtac	tatccgggag	tcacacggcg	ggtgctaacg	tccgtcgtgg
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1141	tgtggaaatc	caaaaacaac	caggaggttg	gcttagaagc	agccatcctt	taaagaaagc
1201	gtaacagctc	actggtctaa	ataagggttt	ctgcgccgaa	gatgtaacgg	ggctcaagcc
1261	acgagccgaa	gcttaggggtg	tgatccgcaa	gggtcacgcg	gtagcggagc	gttctgtaag
1321	cctgcgaagg	gcgactcgtg	agagcgcctg	gaggtatcag	aagtgcgaat	gctggcatga
1381	gtaacgacaa	acactgtgaa	agacagtgtc	gccgaaagtc	caagggttcc	tgcgtaaagt
1441	taatcttcgc	agggtttagcc	ggtccctaag	gcgaggccga	aaggcgtagt	cgatgggaat
1501	gcagtgaata	ttctgcagcc	agtggatggg	gacgaatccc	gtgtgttgtc	cgaccttact
1561	ggattgggtg	ggcttcgaag	gggttccagg	aaatagcctc	cacatcagac	cgtacccgaa
1621	accgacacag	gtggactggg	agagtatacc	aaggcgattg	agagaactat	gttgaaggaa
1681	ctcggcaatt	tacctccgta	acttcgggat	aaggaggccc	attgctcgcg	caagcgggca
1741	gtggggggcac	agaccagggg	gtggcaactg	tttaacaaaa	acacagggct	ctgcgaaatc
1801	gcaagatgac	gtataggggtc	tgacgcctgc	ccggtgccgg	aagggttaaga	ggagaggtgc
1861	aagccttgaa	tcgaagcccc	ggtaaacggc	ggccgtaact	ataacgggtcc	taaggtagcg
1921	aaatttccttg	tcgggttaagt	tccgacctgc	acgaatggcg	taatgacttc	cccgtgtctt
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2101	aataggtggg	aggctttgaa	gccgtggcgc	cagccatggg	ggagccgaaa	tgtgaaatac
2161	caccctaattg	gttatggata	tctaaccgcg	ttccctcagc	ggggaccggg	acagcgcag
2221	gtgggcagtt	tgactggggc	ggtcgcctcc	caaagagtaa	cggaggcgtg	cgaaggtagg
2281	ctcagaacgg	tcggaaatcg	ttcgtcgagt	ataatggcat	aagcctgcct	gactgcgaga
2341	tctacgaatc	gagcagagac	gaaagtcggg	catagtgatc	cgggtggccc	gcgtggatgg
2401	gccatcgctc	aacggataaa	aggtacgccg	gggataacag	gctgatgacg	ccaagagtc
2461	catatcgacg	gcgtcgtttg	gcacctcgat	gtcggctcat	cacatcctgg	ggctggagaa
2521	ggtcccaagg	gttcggctgt	tcgccgatta	aagtggtagc	tgagctgggt	tcagaacgtc
2581	gtgagacagt	tcggtcctta	tctgccgtgg	gtgttggaa	gttgagagga	tttgccccta
2641	gtacgagagg	accgggggtga	acgtacctct	ggtggagctg	ttgtcgcgcc	agcggcagtg
2701	cagcatagct	atgtacggac	gggataaccg	ctgaaagcat	ctaagcggga	aaccacctc
2761	aaaacgagca	ttcccttgag	aaccgtggaa	gaccaccacg	ttgataggcc	gggtgtggaa
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2881	tt					

=>

Use of real-time PCR and

fluorimetry for rapid detection of rifampin and isoniazid resistance-associated mutations in *Mycobacterium tuberculosis*

AUTHOR: TORRES M. J.; CRIADO A.; PALOMARES J. C.; AZNAR J.  
CORPORATE SOURCE: Unidad de Microbiología Molecular, Departamento de Microbiología, Universidad de Sevilla, 41080 Sevilla, Spain  
SOURCE: Journal of clinical microbiology, (2000), 38(9), 3194-3199, 24 refs.  
ISSN: 0095-1137 CODEN: JCMIDW  
DOCUMENT TYPE: Journal  
BIBLIOGRAPHIC LEVEL: Analytic  
COUNTRY: United States  
LANGUAGE: English  
AVAILABILITY: INIST-17088, 354000091289690100  
AN 2000-0532525 PASCAL  
CP Copyright .COPYRG. 2000 INIST-CNRS. All rights reserved.  
AB Very fast amplification of DNA in small volumes can be continuously monitored with a rapid cyclor that incorporates fluorimetric detection. Primers were designed to amplify a 157-bp fragment of the *rpoB* gene spanning codons 526 and 531 and a 209-bp fragment of the *katG* gene spanning codon 315 of *Mycobacterium tuberculosis*. Most mutations associated with resistance to rifampin (RMP) and isoniazid (INH) in clinical isolates occur in these codons. Two pairs of hybridization probes were synthesized; one in each pair was 3' labeled with fluorescein and hybridized upstream of the codon with the mutation; the other two probes were 5' labeled with LightCycler-Red 640. Each pair of probes recognized adjacent sequences in the amplicon. After DNA amplification was finished by using a LightCycler, the temperature at which the Red 640 probe melted from the product was determined in a 3-min melt program. Twenty *M. tuberculosis* clinical isolates susceptible to streptomycin, INH, RMP, and ethambutol and 36 antibiotic-resistant clinical *M. tuberculosis* isolates (16 resistant to RMP, 16 to INH, and 4 to both antimicrobial agents) were amplified, and the presence of mutations was determined using single-strand conformation polymorphism analysis, the LiQor automated sequencer, and the LightCycler system. Concordant results were obtained in all cases. Within 30 min, the LightCycler method correctly genotyped all the strains without the need of any post-PCR sample manipulation. Overall, this pilot study demonstrated that real-time PCR coupled to fluorescence detection is the fastest available method for the detection of RMP and INH resistance-associated mutations in *M. tuberculosis* clinical isolates.

L5 ANSWER 23 OF 31 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:418561 SCISEARCH  
THE GENUINE ARTICLE: 814GK  
TITLE: Direct detection of rifampin- and isoniazid-resistant *Mycobacterium tuberculosis* in auramine-rhodamine-positive sputum specimens by real-time PCR  
AUTHOR: Ruiz M; Torres M J (Reprint); Llanos A C; Arroyo A; Palomares J C; Aznar J  
CORPORATE SOURCE: Fac Med, Dept Microbiol, Apdo 914, Sevilla 41080, Spain (Reprint); HH UU Virgen del Rocío, Microbiol Serv, Sevilla, Spain; Univ Sevilla, Unidad Microbiol Mol, Dept Microbiol, Sevilla, Spain  
COUNTRY OF AUTHOR: Spain  
SOURCE: JOURNAL OF CLINICAL MICROBIOLOGY, (APR 2004) Vol. 42, No. 4, pp. 1585-1589.  
ISSN: 0095-1137.

PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC  
20036-2904 USA.  
DOCUMENT TYPE: Article; Journal  
LANGUAGE: English  
REFERENCE COUNT: 30  
ENTRY DATE: Entered STN: 21 May 2004  
Last Updated on STN: 21 May 2004

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Our objective was to evaluate the feasibility of a molecular assay based on a real-time PCR technique, carried out with a LightCycler instrument (Roche Biochemicals), to identify *Mycobacterium tuberculosis* bacilli and to detect rifampin and isoniazid resistance in DNA extracts from sputum samples. We studied three genes: *rpoB*, which is associated with rifampin resistance, and *katG* and *inhA*, which are associated with isoniazid resistance. A total of 205 sputum samples collected from 108 patients diagnosed with pulmonary tuberculosis with positive auramine-rhodamine-staining (AR) sputum samples, were tested. The sensitivities of the LightCycler PCR assay for the positive AR specimens was 97.5% (200 of 205) for *rpoB* and *inhA* genes and 96.5% (198 of 205) for the *katG* gene. For the total number of patients tested, the sensitivity was 100% (108 of 108 patients) for rifampin, whereas the sensitivity was 98.1% (106 of 108 patients) for isoniazid. Full agreement was found with the Bactec MGIT 960 method and the genotype inferred from the LightCycler data for rifampin. The phenotypic method for isoniazid reported 13 resistant strains (greater than or equal to 0.1 µg/ml). In seven (53.8%) strains there was a concordance between both methods, but we found that six (46.2%) strains reported as resistant by the phenotypic method were determined to be susceptible by real-time PCR. For the 75 strains reported as susceptible by the phenotypic method, the concordance with the LightCycler data was 100%. Our results demonstrate that rifampin-resistant *M. tuberculosis* could be detected in DNA extracted from auramine-rhodamine-positive sputum samples in a single-tube assay that took less than 3 h to perform for a collection of auramine-rhodamine-positive specimens obtained from patients with culture-documented pulmonary tuberculosis. Similarly, this occurs in half of the isoniazid-resistant *M. tuberculosis* DNA extracted from auramine-rhodamine-positive specimens.

FILE 'MEDLINE, AGRICOLA, ANTE, AQUALINE, BIOSIS, BIOTECHNO, CABA, CAPLUS, CBNB, CIN, CONFSCI, CROPB, CROPU, DISSABS, ENVIROENG, ESBIODASE, FOMAD, FOREGE, FROSTI, FSTA, GENBANK, IFIPAT, INVESTEXT, LIFESCI, NAPRALERT, NTIS, PASCAL, PHIC, PHIN, PROMT, ...' ENTERED AT 15:53:46 ON 31 JUL 2006

L1 303119 S (BRADYRHIZOBIUM OR JAPONICUM OR RHIZOBIUM)  
L2 85 S L1 AND ((REAL-TIME PCR) OR (REAL TIME (3A) POLYMERASE CHAIN  
L3 59 DUP REM L2 (26 DUPLICATES REMOVED)

=> d l3 ti 1-59

L3 ANSWER 1 OF 59 USPATFULL on STN  
TI Receptors and membrane-associated proteins

L3 ANSWER 2 OF 59 USPATFULL on STN  
TI Treatment of fibrosis using FXR ligands

L3 ANSWER 3 OF 59 USPATFULL on STN  
TI Molecules for disease detection and treatment

L3 ANSWER 4 OF 59 USPATFULL on STN  
TI Genus, group, species and/or strain specific 16S rDNA sequences

L3 ANSWER 5 OF 59 USPATFULL on STN  
TI Nucleic acid and polypeptide sequences from *Lawsonia intracellularis* and methods of using

L3 ANSWER 6 OF 59 USPATFULL on STN  
TI Identification of novel e2f target genes and use thereof

L3 ANSWER 7 OF 59 USPATFULL on STN  
TI Genomic barcoding for organism identification

L3 ANSWER 8 OF 59 USPATFULL on STN  
TI Proteome epitope tags and methods of use thereof in protein modification analysis

L3 ANSWER 9 OF 59 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN  
TI Transcriptome profiling of lung schistosomula, in vitro cultured schistosomula and adult *Schistosoma japonicum*;  
lung schistosomula, in vitro cultured schistosomula and adult *Schistosoma japonicum* transcriptome expression profiling for transcriptomics

L3 ANSWER 10 OF 59 MEDLINE on STN DUPLICATE 1  
TI Dynamics of CD4+CD25+ T cells in spleens and mesenteric lymph nodes of mice infected with *Schistosoma japonicum*.

L3 ANSWER 11 OF 59 Elsevier BIOBASE COPYRIGHT 2006 Elsevier Science B.V. on STN  
TI The transformation of betaA gene into the pollen plantlets of *Populus simoniixP. nigra*

L3 ANSWER 12 OF 59 MEDLINE on STN DUPLICATE 2  
TI Design and validation of a partial-genome microarray for transcriptional profiling of the *Bradyrhizobium japonicum* symbiotic gene region.

L3 ANSWER 13 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3  
TI Isolation and mutagenesis of broad host range pBBR1-based plasmids having altered plasmid copy number

L3 ANSWER 14 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN DUPLICATE 4  
TI BROAD HOST RANGE PBBR1-BASED PLASMID MUTANT DERIVATIVES HAVING ALTERED

PLASMID COPY NUMBER

L3 ANSWER 15 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN  
TI Identification of Rhizobium species clogging activated sludge separation membrane based on 16S rRNA gene sequence

L3 ANSWER 16 OF 59 USPATFULL on STN  
TI Small molecule and peptide arrays and uses thereof

L3 ANSWER 17 OF 59 USPATFULL on STN  
TI Gene products differentially expressed in cancerous cells and their methods of use II

L3 ANSWER 18 OF 59 USPATFULL on STN  
TI Protein modification and maintenance molecules

L3 ANSWER 19 OF 59 USPATFULL on STN  
TI Compositions and methods for treating diseases

L3 ANSWER 20 OF 59 USPATFULL on STN  
TI Enzymes

L3 ANSWER 21 OF 59 USPATFULL on STN  
TI Nucleic acid-associated proteins

L3 ANSWER 22 OF 59 USPATFULL on STN  
TI Kinases and phosphatases

L3 ANSWER 23 OF 59 USPATFULL on STN  
TI Protein

L3 ANSWER 24 OF 59 USPATFULL on STN  
TI Secreted proteins

L3 ANSWER 25 OF 59 USPATFULL on STN  
TI Enzymes

L3 ANSWER 26 OF 59 USPATFULL on STN  
TI Compositions and methods for treating inflammatory disorders

L3 ANSWER 27 OF 59 USPATFULL on STN  
TI Receptors and membrane-associated proteins

L3 ANSWER 28 OF 59 USPATFULL on STN  
TI Protein modification and maintenance molecules

L3 ANSWER 29 OF 59 USPATFULL on STN  
TI Therapeutic treatment methods 2

L3 ANSWER 30 OF 59 USPATFULL on STN  
TI Manipulation of flavonoid biosynthesis in plants

L3 ANSWER 31 OF 59 USPATFULL on STN  
TI Proteins associated with cell growth, differentiation, and death

L3 ANSWER 32 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN  
TI Transcript enrichment of Nod factor-elicited early nodulin genes in purified root hair fractions of the model legume Medicago truncatula.

L3 ANSWER 33 OF 59 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN  
TI Techniques for detecting genetically modified crops and products.

L3 ANSWER 34 OF 59 Elsevier BIOBASE COPYRIGHT 2006 Elsevier Science B.V.  
on STN  
TI Expression levels of avrBs3-like genes affect recognition specificity in  
tomato Bs4- but not in pepper Bs3-mediated perception

L3 ANSWER 35 OF 59 MEDLINE on STN DUPLICATE 5  
TI Symbiotic and saprophytic survival of three unmarked Rhizobium  
leguminosarum biovar trifolii strains introduced into the field.

L3 ANSWER 36 OF 59 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights  
reserved on STN  
TI Directed evolution of copy number of a broad host range plasmid for  
metabolic engineering.

L3 ANSWER 37 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 6  
TI Assays and devices for detecting microbial contamination in animal  
by-products

L3 ANSWER 38 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN DUPLICATE 7  
TI QUANTITATIVE ASSAY FOR THE SIMULTANEOUS DETECTION AND SPECIATION OF  
BACTERIAL INFECTIONS

L3 ANSWER 39 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN  
TI QUANTITATIVE ASSAY FOR THE SIMULTANEOUS DETECTION AND SPECIATION OF  
BACTERIAL INFECTIONS; ADAPTATION OF THE REAL-TIME  
PCR ASSAY ALLOWS FOR HIGHLY SENSITIVE DETECTION OF ANY  
EUBACTERIAL SPECIES WITH SIMULTANEOUS SPECIATION. THE ASSAY RELIES ON A  
'MULTIPROBE' DESIGN IN WHICH A SINGLE SET OF HIGHLY CONSERVED SEQUENCES

L3 ANSWER 40 OF 59 USPATFULL on STN  
TI Vesicle-associated proteins

L3 ANSWER 41 OF 59 USPATFULL on STN  
TI Adiponectin receptor and gene encoding the same

L3 ANSWER 42 OF 59 USPATFULL on STN  
TI Detecting microbial contamination in grain and related products

L3 ANSWER 43 OF 59 USPATFULL on STN  
TI Compositions and methods for treating neurological disorders and  
diseases

L3 ANSWER 44 OF 59 USPATFULL on STN  
TI Compositions and methods for treating diabetes

L3 ANSWER 45 OF 59 USPATFULL on STN  
TI Methods for improving plant agronomical traits by altering the  
expression or activity of plant G-protein alpha and beta subunits

L3 ANSWER 46 OF 59 USPATFULL on STN  
TI Cpn60 targets for quantification of microbial species

L3 ANSWER 47 OF 59 USPATFULL on STN  
TI Detecting hormonally active compounds

L3 ANSWER 48 OF 59 USPATFULL on STN  
TI Detection and quantification of aromatic oxygenase genes by real  
-time PCR

L3 ANSWER 49 OF 59 USPATFULL on STN  
TI Therapeutic treatment methods

L3 ANSWER 50 OF 59 USPATFULL on STN  
 TI Method of selecting antimicrobial agent and method of using the same

L3 ANSWER 51 OF 59 USPATFULL on STN  
 TI Monitoring high-risk environments

L3 ANSWER 52 OF 59 MEDLINE on STN DUPLICATE 8  
 TI Highly up-regulated CXCR3 expression on eosinophils in mice infected with *Schistosoma japonicum*.

L3 ANSWER 53 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN  
 TI Expression of hemoglobin genes in actinorhizal plant (non-leguminous plant symbiosis with *Frankia*)

L3 ANSWER 54 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN DUPLICATE 9  
 TI QUANTITATIVE ASSAY FOR THE SIMULTANEOUS DETECTION AND SPECIATION OF BACTERIAL INFECTIONS; ADAPTATION OF THE REAL-TIME PCR ASSAY ALLOWS FOR HIGHLY SENSITIVE DETECTION OF ANY EUBACTERIAL SPECIES WITH SIMULTANEOUS SPECIATION. THE ASSAY RELIES ON A 'MULTIPROBE' DESIGN IN WHICH A SINGLE SET OF HIGHLY CONSERVED SEQUENCES

L3 ANSWER 55 OF 59 USPATFULL on STN DUPLICATE 10  
 TI *Histoplasma capsulatum* catalase sequences and their use in the detection of *Histoplasma capsulatum* and Histoplasmosis

L3 ANSWER 56 OF 59 MEDLINE on STN  
 TI Pleiotropic effect of the insertion of the *Agrobacterium rhizogenes* rolD gene in tomato (*Lycopersicon esculentum* Mill.).

L3 ANSWER 57 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN  
 TI Highly up-regulated CXCR3 expression on eosinophils in mice infected with *Schistosoma japonicum*

L3 ANSWER 58 OF 59 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN  
 TI Detecting and determining species source of eubacterial DNA in a sample, comprises amplifying template DNA in the sample using a real-time polymerase chain reaction with the use of primers and at least two fluorogenic probes; bacterium DNA detection and polymerase chain reaction

L3 ANSWER 59 OF 59 USPATFULL on STN  
 TI Modulation of mitochondrial mass and function for the treatment of diseases and for target and drug discovery

=>

Proteomic analysis of soybean root hairs after infection

by Bradyrhizobium japonicum

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CORPORATE SOURCE: Univ Missouri, Natl Ctr Soybean Biotechnol, Dept Microbiol  
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\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Infection of soybean root hairs by Bradyrhizobium  
japonicum is the first of several complex events leading to  
nodulation. In the current proteomic study, soybean root hairs after  
inoculation with B. japonicum were separated from roots. Total proteins  
were analyzed by two-dimensional (2-D) polyacrylamide gel electrophoresis.  
In one experiment, 96 protein spots were analyzed by matrix-assisted laser  
desorption ionization time-of-flight (MALDI-TOF) mass spectrometry (MS) to  
compare protein profiles between uninoculated roots and root hairs.  
Another 37 spots, derived from inoculated root hairs over different  
timepoints, were also analyzed by tandem NIS (MS/MS). As expected, some  
proteins were differentially expressed in root hairs compared with roots  
(e.g., a chitinase and phosphoenolpyruvate carboxylase). Out of 37 spots  
analyzed by MS/MS, 27 candidate proteins were identified by database  
comparisons. These included several proteins known to respond to  
rhizobial inoculation (e.g., peroxidase and phenylalanine-ammonia lyase).  
However, novel proteins were also identified (e.g., phospholipase D and  
phosphoglucosyltransferase). This research establishes an excellent system for  
the study of root-hair infection by rhizobia and, in a more general sense,  
the functional genomics of a single, plant cell type. The results  
obtained also indicate that proteomic studies with soybean, lacking a  
complete genome sequence, are practical.

=> end

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TITLE: Identification of Rgg-regulated exoproteins of *Streptococcus pyogenes*.  
AUTHOR: Chaussee M S; Watson R O; Smoot J C; Musser J M  
CORPORATE SOURCE: Laboratory of Human Bacterial Pathogenesis, Rocky Mountain Laboratories, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, Montana 59840, USA.  
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AB *Streptococcus pyogenes* secretes many proteins that influence host-pathogen interactions. Despite their importance, relatively little is known about the regulation of these proteins. The *rgg* gene (also known as *ropB*) is required for the expression of streptococcal erythrogenic toxin B (SPE B), an extracellular cysteine protease that contributes to virulence. Proteomics was used to determine if *rgg* regulates the expression of additional exoproteins. Exponential- and stationary-phase culture supernatant proteins made by *S. pyogenes* NZ131 *rgg* and NZ131 *speB* were separated by two-dimensional electrophoresis. Differences were identified in supernatant proteins from both exponential- and stationary-phase cultures, although considerably more differences were detected among stationary-phase supernatant proteins. Forty-two proteins were identified by peptide fingerprinting with matrix-assisted laser desorption mass spectrometry. Mitogenic factor, DNA entry nuclease (open reading frame [ORF 226]), and ORF 953, which has no known function, were more abundant in the culture supernatants of the *rgg* mutant compared to the *speB* mutant. ClpB, lysozyme, and autolysin were detected in the culture supernatant of the *speB* mutant but not the *rgg* mutant. To determine if Rgg affected protein expression at the transcriptional level, real-time (TaqMan) reverse transcription (RT)-PCR was used to quantitate Rgg-regulated transcripts from NZ131 wild-type and *speB* and *rgg* mutant strains. The results obtained with RT-PCR correlated with the proteomic data. We conclude that Rgg regulates the transcription of several genes expressed primarily during the stationary phase of growth.

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